

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 05:09:32 ; Search time 3730 Seconds

(without alignments)  
9368.096 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 918  
Sequence: 1 GAATTCATGAAAAAAGCCG.....ATCACCATTAGTGAAGCTT 918

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Database : EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hlc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_g881:\*  
9: gb\_g882:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	317.6	34.6	584	2	BF664453 602146204
2	315.8	34.4	683	7	CR745461 CR745461
3	314.8	34.3	516	2	AM401728 UI-HF-BKO
4	313.4	34.1	536	2	AM402624 UI-HF-BKO
5	311	33.9	881	5	BQ709375 AGENCOURT
6	310.6	33.8	979	5	BQ709399 AGENCOURT
7	309	33.7	424	2	BF874079 UI-HF-BKO
8	308.6	33.6	566	2	AM405972 UI-HF-BKO
9	308	33.6	745	4	BI759245 603042678
10	307.8	33.5	433	1	AV647117 AV647117
11	307.8	33.5	440	1	AV647111 AV647111
12	307.8	33.5	504	1	AM405787 UI-HF-BKO
13	307.8	33.5	734	4	BG686748 602650717
14	307.8	33.5	793	1	AV646708 AV646708
15	307.8	33.5	926	5	BQ706634 AGENCOURT
16	307.8	33.5	998	5	BQ709245 AGENCOURT
17	306.2	33.4	518	2	AM406576 UI-HF-BKO
18	306.2	33.4	862	4	BG758749 602713108
19	306.2	33.4	1014	5	BM918339 AGENCOURT
20	306	33.3	456	2	AM406451 UI-HF-BKO
21	305.8	33.3	472	2	AM405697 UI-HF-BKO
22	305.8	33.3	603	2	AM404910 UI-HF-BKO
23	304.6	33.2	933	5	BQ711272 AGENCOURT
24	304.2	33.1	526	5	BQ331002 QV3-BT019

25	303.8	33.1	1069	5	BM919414 AGENCOURT
26	303.4	33.1	1153	2	BF663521 602144686
27	303	33.0	441	2	BF914735 UI3-UT011
28	303	33.0	441	2	BF914740 UI3-UT011
29	303	33.0	488	4	BM830796 K-EST0104
30	303	33.0	504	2	BF917294 UI3-UT011
31	303	33.0	529	6	CD708287 EST24814
32	303	33.0	544	2	AM405216 UI-HF-BKO
33	303	33.0	644	2	AM405817 UI-HF-BKO
34	303	33.0	679	6	CD684618 EST1138 h
35	303	33.0	923	5	BQ711051 AGENCOURT
36	303	33.0	974	5	BQ707037 AGENCOURT
37	302.6	33.0	489	2	AM406488 UI-HF-BKO
38	302.6	33.0	579	6	CD707672 EST24199
39	302.4	32.9	865	5	BX357917 BX357917
40	301.8	32.9	976	5	BM914525 AGENCOURT
41	301.4	32.8	978	5	BQ707988 AGENCOURT
42	301	32.8	686	6	CD692160 EST8699 h
43	301	32.8	786	6	CB956522 AGENCOURT
44	301	32.8	917	5	BQ711815 AGENCOURT
45	300.6	32.7	718	6	CB957976 AGENCOURT

## ALIGNMENTS

RESULT 1  
LOCUS BF664453 584 bp mRNA linear EST 21-DEC-2000  
DEFINITION 602146204f NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4309680 5',  
mRNA sequence.

ACCESSION BF664453  
VERSION BF664453.1 GI:11938258  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 584)  
NIH-MGC http://mgs.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1CML183 row: h column: 01  
High quality sequence strop: 584.

## FEATURES

source

1..584  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4309680"  
/tissue\_type="primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_48"  
/note="Organ: B-cells; Vector: pOTB7, Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match	34.6%	Score 317.6	DB 2	Length 584
Best Local Similarity	87.3%	Pred. No. 46-77		
Matches 363	Conservative	0	Mismatches 44	Indels 9
			Gaps	1
QY	15	AACCGTATGCGATGCGAGTTGCACTGGCTGGTTGCTACCGTGGCGCAGGCCGAAAT	74	
Db	17	AAACCCCGAGCCAGCTTCTCTTCCCTCGCTACTCTGGCTCCGATATACACCGGAGAA	76	
QY	75	TGTGTGACGAGTCTCCAGGACCCCTCTTGTCTCAGGAGGAAAGACCACTCTC	134	
Db	77	TGTGTGACGAGTCTCCAGGACCCCTGTCTTGTCTCAGGAGGAAAGACCACTCTC	136	
QY	135	CTGCAGGGCCAGTCAGAGTGTATGAGCAGTACTTACCTGGTACCGAGAGAAACTGG	194	
Db	137	CTGCAGGGCCAGTCAGAGTGTATCCAGAGCTACTTAACCTGGTATCCAGAGAACTGG	196	
QY	195	CCAGGCTCCAGGCTCTCATCTATGTGTGCATCCACGAGGCCACTGGCATCCAGAAC	254	
Db	197	CCAGGCTCCAGGCTCTCATCTATGTGTGCATCCAGAGGGCCACTGGCATCCAGAAC	256	
QY	255	GTTGAGTGGCAGTGGGTCCGGGACAGACTTCATCTCAACATCACTAGCTGGAGCCGGA	314	
Db	257	GTTGAGTGGCAGTGGGTCTGGGACAGACTTCACTTCAACATCACTAGCTGGAGCCGGA	316	
QY	315	AGATTTTGCAGTGTATTACTGTCTACGACGATATGTAGTCACTCAGACCTCAGACTAC	374	
Db	317	AGATTTTGCAGTGTATTACTGTCTACGACGATATGATGAT-----CACCTCCGAGAAC	367	
QY	375	TTTGGCGGAGAGGACCAAGGTGGAGATCAAAAGAACTGGTGTGACATCTGTCT	430	
Db	368	TTTGGCGGAGAGGACCAAGGTGGAGATCAAAAGAACTGGTGTGACATCTGTCT	423	

FEATURES	source
RESULT 2	
LOCUS	CR745461
DEFINITION	CR745461 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
ACCESSION	U00000.1
VERSION	CR745461.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 683) Ebert,J., Heil,O., Hennig,S., Korn,B., Neubert,P., Patsch,E., Peters,M., Radelof,U. and Schneider,D. I.M.A.G.E. cDNA Clone Collection Unpublished (2004)
TITLE	Contact: Inge Ariart
JOURNAL	RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
COMMENT	Heubnerweg 6, D-14059 Berlin, Germany Email: www.rzpd.de RZPD; IMAG971P116. RZPDLIB; I.M.A.G.E. cDNA Clone Collection; Contact: Inge Ariart RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 100 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD, contact RZPD (clone@rzpd.de) for further information. Seq primer: M1r, primer sequence: TTTCACACAGAAACACTATGAC. Location/Qualifiers 1..683

```
Location/Qualifiers
1. .683
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone=IMAGE971P116 ; IMAGE:128434"
/sex="male"
dev_stage="20 week-post conception fetus"
```

ORIGIN

```

/lab host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen mFLs"
/note="Organ: Liver and Spleen; Vector: pTV73D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' AACGTGAGACAGATTAATTAAGAAGCTCTTTTCTTTTCTTTTCTTTT
3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pTV73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

```

Query Match	Score	DB 7	Length	683
Best Local Similarity	94.7%	Pred. No.	1.3e-76	
Matches	342	Conservative	0	Mismatches 7
			Indels	12
			Gaps	1
Oy	70	GATATGTGTGACGACAGCTCTCCAGGACCCCTGTCTTGTGTCTCCAGGGGAAAAGACCA	129	
Db	58	GAAATGTGTGACGACAGCTCTCCAGGACCCCTGTCTTGTGTCTCCAGGGGAAAAGACCA	117	
Oy	130	CTCTCCGACAGGCGACGTCAAGTGTATGTATGACAGCTTAAAGCTTGSTATCCAGAGAA	189	
Db	118	CTCTCTGACAGGCGACGTCAAGTGTATGTATGACAGCACTTAAGCTTGSTATCCAGAGAA	177	
Oy	190	CCTGGCCAGGCTCCAGGCTCCTCATCTATGATGATCATCACAGGGCCACTGGCATGCA	249	
Db	178	CCTGGCCAGGCTCCAGGCTCCTCATCTATGATGATCATCACAGGGCCACTGGCATGCCA	237	
Oy	250	GACAGGTTCAGTGGGAGTGGGTCGGGACAGACTTCACTCTACCATATAGTAACTGGAG	309	
Db	238	GACAGGTTCAGTGGGAGTGGGTCGGGACAGACTTCACTCTACCATATAGAGACTGGAG	297	
Oy	310	CCTAAGATTTTGGAGTATATTATCTGTACAGAGTATGGTAGCTCAACCTCAAGACCTCAG	369	
Db	298	CCTAAGATTTTGGAGTATATTATCTGTACAGAGTATGGTAGCTCAAC-----G	345	
Oy	370	ATCACTTTCCGCGAGGAGCCAAAGGTGAGATCAAAAGAACTGTGGCTGACCAATCTGTG	429	
Db	346	CTCACTTTCCGCGAGGAGCCAAAGGTGAGATCAAAAGAACTGTGGCTGACCAATCTGTG	405	
Oy	430	T	430	
Db	406	T	406	

RESULT 3	516 bp	mRNA	linear	EST 16-FEB-2000
LOCUS	AM401728			
DEFINITION	UI-HF-BK0-aaf-f-12-0-UI.r1 NIH-MGC-36 Homo sapiens cDNA clone IMAGE:3053711 5', mRNA sequence.			
ACCESSION	AM401728			
VERSION	AM401728.1			
KEYWORDS	GI:6920414			
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
REFERENCE	Homo sapiens			
AUTHORS	Emkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
TITLE	1 (bases 1 to 516)			
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: <a href="mailto:cgapsb@emil.nih.gov">cgapsb@emil.nih.gov</a>			
	EST. RI site shown at the beginning of the sequence.			
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.			
	cDNA Library Preparation: Louis M. Staudt, M.D., Ph.D.			
	cDNA Library Arrayed by: M.B. Soares Lab			
	DNA Sequencing by: M.B. Soares Lab			
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:			
	<a href="http://www.bio.linnl.gov/bdrrp/image/image.html">www.bio.linnl.gov/bdrrp/image/image.html</a>			
	Seq primer: M13 forward.			

FEATURES  
source

Location/Qualifiers  
1..516  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3053711"  
/issue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LT1)"  
/clone\_11b="NIH MGC 36"  
/note="Vector: pTV73-Pac; Site 1: NotI; Site 2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(0.5-1.5kb). Directionally cloned. Cells provided by Louis  
M. Staedt, Ph.D. Library preparation by Maria de Fatima  
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

## ORIGIN

Query Match 34.1%; Score 314.8; DB 2; Length 516;  
Best Local Similarity 85.8%; Pred. No. 2,3e-76;  
Matches 362; Conservative 0; Mismatches 57; Indels 3; Gaps 1;

440 GCGGTTCCGAGAGTGTGATCAGTGAAGTGGCTCCAGGTGACGTGAGAGTCTG 499  
93 GGGTTTCTCTGCTCTTTAAGAGTGTCCAGTGTGACGTGAGTGTGAGTCTG 152  
500 GGGAGGCGGTGTCAGCCTGGAGGTCCTTGAGACTCTCTGTGAGCCTTGATTCC 559  
153 GGGAGGCGGTGTCAGCCTGGAGGTCCTTGAGACTCTCTGTGAGCCTTGATTCA 212  
560 CTTTCAAGAGCTTTGATGACATGAGTCCGACGCTTGAAGCAAGGGGCTGAGTGG 619  
213 CTTTCAAGTGTATGATGACATGAGTCCGACGCTTGAAGCAAGGGGCTGAGTGG 272  
620 TGGAGTTATCATATGATGAGCACTAAATACAGCAGACTCCGTGAAGGGCCGAT 679  
273 TGGAGTTATCATATGATGAGCACTAAATACAGCAGACTCCGTGAAGGGCCGAT 332  
680 TCACCATCTCCAGAGACCTTCCAGAACACGGTGTATCTAAATGAACAGCTGAGAA 739  
333 TCACCATCTCCAGAGACCTTCCAGAACACGGTGTATCTGCAATGAACAGCTGAGAA 392  
740 CTGAGAGACAGGCTGTCTTACTGTCGAGAGATGAGAGCC---TGTGGGAGACTAG 796  
393 CTGAGAGACAGGCTGTCTTACTGTCGAGAGATGAGAGCC---TGTGGGAGACTAG 452  
797 ACCACTACTACGAGTTGAGAGCTCTGGGCAAGAGGACACGGTCAACGCTCTCTGAGAT 856  
453 ACTACTACTACGAGTTGAGAGCTCTGGGCAAGAGGACACGGTCAACGCTCTCTGAGCTT 512  
857 CC 858  
513 CC 514

RESULT 4  
AM402624 536 bp mRNA linear EST 16-FEB-2000  
LOCUS UI-HF-BKO-sax-h-08-0-UI\_r1 NIH MGC\_36 Homo sapiens cDNA clone  
DEFINITION IMAGE:3055359 5', mRNA sequence.  
ACCESSION AM402624 GI:6921329  
VERSION AM402624  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE 1 (bases 1 to 536)  
JOURNAL NIH-MGC http://mgi.nci.nih.gov/  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

FEATURES  
source

Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staedt, M.D., Ph.D.  
CDNA Library Preparation: M.B. Soares Lab  
CDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNL at:  
www.bio.lnl.gov/birdp/image/image.html  
Seq primer: M13 forward.

## ORIGIN

Query Match 34.1%; Score 313.4; DB 2; Length 536;  
Best Local Similarity 85.9%; Pred. No. 5.8e-76;  
Matches 360; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

440 GCGGTTCCGAGAGTGTGATCAGTGAAGTGGCTCCAGGTGACGTGAGAGTCTG 499  
57 GGGTTTCTCTGCTCTTTAAGAGTGTCCAGTGTGACGTGAGTGTGAGTCTG 116  
500 GGGAGGCGGTGTCAGCCTGGAGGTCCTTGAGACTCTCTGTGAGCCTTGATTCC 559  
117 GGGAGGCGGTGTCAGCCTGGAGGTCCTTGAGACTCTCTGTGAGCCTTGATTCA 176  
560 CTTTCAAGAGCTTTGATGACATGAGTCCGACGCTTGAAGCAAGGGGCTGAGTGG 619  
177 CTTTCAAGTGTATGATGACATGAGTCCGACGCTTGAAGCAAGGGGCTGAGTGG 236  
620 TGGAGTTATCATATGATGAGCACTAAATACAGCAGACTCCGTGAAGGGCCGAT 679  
237 TGGAGTTATCATATGATGAGCACTAAATACAGCAGACTCCGTGAAGGGCCGAT 296  
680 TCACCATCTCCAGAGACCTTCCAGAACACGGTGTATCTAAATGAACAGCTGAGAA 739  
297 TCACCATCTCCAGAGACCTTCCAGAACACGGTGTATCTGCAATGAACAGCTGAGAA 356  
740 CTGAGAGACAGGCTGTCTTACTGTCGAGAGATGAGAGCC---TGTGGTGTGACTAGAC 799  
357 CTGAGAGACAGGCTGTCTTACTGTCGAGAGATGAGAGCC---TGTGGTGTGACTAG 413  
800 ACTACTACGAGTTGAGAGCTCTGGGCAAGAGGACACGGTCAACGCTCTCTGAGATCC 858  
414 ACTACTACGAGTTGAGAGCTCTGGGCAAGAGGACACGGTCAACGCTCTCTGAGCTCC 472

RESULT 5  
BQ709375 881 bp mRNA linear EST 16-JUL-2002  
LOCUS AGENCOURT 7977299 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6215729  
DEFINITION 5', mRNA sequence.  
ACCESSION BQ709375 GI:21848274  
VERSION BQ709375  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE 1 (bases 1 to 881)  
JOURNAL NIH-MGC http://mgi.nci.nih.gov/  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
Plate: LNCM385 row: b column: 18  
High quality sequence stop: 700.  
Location/Qualifiers

## FEATURES

source  
1. .881  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6215729"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 33.9%; Score 311; DB 5; Length 881;  
Best Local Similarity 93.9%; Pred. No. 3e-75;  
Matches 339; Conservative 0; Mismatches 10; Indels 12; Gaps 1;

```
QY 70 GATATTGTGTGACGAGCTCCAGGACCCCTGTTGCTCCAGGGGAAAGGCCACC 129
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 130 CTCTCTGCGAGGGCCAGTCAAGTGTAGAGAGCTACTTAACTGTGACAGAGAAA 189
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 190 CCTGGCCAGGCTCCAGGCTCCATCTATGTGTCATCCAGGGCCACTGGCATGCCA 249
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 250 GACAGGTTCACTGGCAGTGGGTCCGGGACAGACTTCACTCCATCAGTGAAGTGGAG 309
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 310 CCTGAAGATTTTGACGTGATTACTGTCAAGCACTATGTAGCTCACTCAGACCTCGA 369
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 370 ATCACTTTGGCGGAGGACCAAGGTGAGATCAAAAGCAATGTGGCTGACCATCTGTC 429
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 430 T 430
DB 418 T 418
```

RESULT 6  
LOCUS BQ709399 979 bp mRNA linear EST 16-JUL-2002  
DEFINITION AGENCOURT\_7977270 NIH\_MGC\_113 Homo sapiens CDNA clone IMAGE:6215847  
ACCESSION BQ709399  
VERSION BQ709399.1 GI:21848298  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
1 (bases 1 to 979)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
Plate: LNCM385 row: g column: 16  
High quality sequence stop: 401.  
Location/Qualifiers

## FEATURES

source  
1. .979  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6215847"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 33.8%; Score 310.6; DB 5; Length 979;  
Best Local Similarity 93.6%; Pred. No. 4e-75;  
Matches 338; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

```
QY 70 GATATTGTGTGACGAGCTCCAGGACCCCTGTTGCTCCAGGGGAAAGGCCACC 129
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 80 GAAATTGTGTGACGAGCTCCAGGACCCCTCTTGTGTCCAGAGAGAGGCCACC 139
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 130 CTCTCTGCGAGGGCCAGTCAAGTGTAGAGAGCTACTTAACTGTGACAGAGAAA 189
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 140 CTCTCTGCGAGGGCCAGTCAAGTGTAGAGAGCTACTTAACTGTGATCAGAGAAA 199
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 190 CCTGGCCAGGCTCCAGGCTCCATCTATGTGTCATCCAGGGCCACTGGCATGCCA 249
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 200 CCTGGCCAGGCTCCAGGCTCCATCTATGTGTCATCCAGGGCCACTGGCATGCCA 259
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 250 GACAGGTTCACTGGCAGTGGGTCCGGGACAGACTTCACTCAACATCAGTGAAGTGGAG 309
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 260 GACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCAACATCAGTGAAGTGGAG 319
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 310 CCTGAAGATTTTGACGTGATTACTGTCAAGCACTATGTAGCTCACTCAGACCTCGA 369
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 320 CCTGAAGATTTTGACGTGATTACTGTCAAGCACTATGTAGCTCACTCAGACCTCGA 370
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 370 ATCACTTTGGCGGAGGACCAAGGTGAGATCAAAAGCAATGTGGCTGACCATCTGTC 429
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 430 T 430
DB 431 T 431
```

RESULT 7  
LOCUS BF874079 424 bp mRNA linear EST 17-JAN-2001  
BF874079



DEFINITION IL3-ET0115-071100-302-D08 ET0115 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BP874079  
VERSION BP874079.1 GI:12264209  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mammalia; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 424)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, M. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, D. F., de Souza, S. J. and Simpson, A. J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
10737800  
JOURNAL MEDLINE PubMed  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL3&c2=IL3-ET0115-071100-302-D08&c3=2000-11-07&c4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 392.  
Location/Qualifiers  
1..424  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_1lb="ET0115"  
/note="Organ: Lung tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
ORIGIN  
Query Match 33.7%; Score 309; DB 2; Length 424;  
Best Local Similarity 93.4%; Pred. No. 9, 3e-75;  
Matches 337; Conservative 0; Mismatches 15; Indels 9; Gaps 1;  
QY 70 GATATTGCTTGAAGCAGCTCCAGCACCCTGCTTTTCTCCAGGGAGAGCCACC 129  
DB 61 GAAATTGTTTACGACGAGCTCCAGCACCCTGCTTTTCTCCAGGGAGAGCCACC 120  
QY 130 CTCTCTCAGAGGCGCAGTGTAGTGTAGCAGCTTGTAGCCGTGTACAGCAGAAA 189  
DB 121 CTCTCTCAGAGGCGCAGTGTAGTGTAGCAGCTTGTAGCCGTGTACAGCAGAAA 180  
QY 190 CTGAGCAGGCTCCAGGCTCTCATCTATGTGTATCCAGCAGGCGCATGCGCATGCCA 249  
DB 181 CTGAGCAGGCTCCAGGCTCTCATCTATGTGTATCCAGCAGGCGCATGCGCATGCCA 240  
QY 250 GACAGGTTCAAGGCGAGGCGGCTCCGAGAGAGACTTCACTCAACATCATAGTGAAG 309  
DB 241 GACAGGTTCAAGGCGAGGCGGCTCCGAGAGAGACTTCACTCAACATCATAGTGAAG 300  
QY 310 CCTGAAGATTTTGCAGTGTATTACTGTGCAGAGTATGTAGCTCACTCAGACCTCGAC 369  
DB 301 CCTGAAGATTTTGCAGTGTATTACTGTGCAGAGTATGTAGCTCACTCAGACCTCGAC 351

QY 370 ATCACTTTGGCGGAGGAGCAAGTGTGATCAACGACTGTGGCTGCACCATCTGTC 429  
DB 352 CTCACCTTTCGGCGGAGGAGCAAGTGTGATCAACGACTGTGGCTGCACCATCTGTC 411  
QY 430 T 430  
DB 412 T 412  
RESULT 8  
AM405972  
LOCUS  
DEFINITION AM405972 566 bp mRNA linear EST 16-FEB-2000  
UI-HF-BL0-acy-a-01-0-UI-r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
IMAGE:3060360 5', mRNA sequence.  
ACCESSION AM405972  
VERSION AM405972.1 GI:6925029  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 566)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-riemail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
cDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at:  
www.bio.lnl.gov/bbrp/image/image.html  
Seq primer: M13 forward  
Location/Qualifiers  
1..566  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_1imgb="3060360"  
/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (UTi)"  
/clone\_1lb="NIH MGC 37"  
/note="Vector: pRTT3-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."  
ORIGIN  
Query Match 33.6%; Score 308.6; DB 2; Length 566;  
Best Local Similarity 93.1%; Pred. No. 1, 3e-74;  
Matches 336; Conservative 0; Mismatches 19; Indels 6; Gaps 1;  
QY 70 GATATTGCTTGAAGCAGCTCCAGCACCCTGCTTTTCTCCAGGGAGAGCCACC 129  
DB 66 GAAATTGTTTACGACGAGCTCCAGCACCCTGCTTTTCTCCAGGGAGAGCCACC 125  
QY 130 CTCTCTCAGAGGCGCAGTGTAGTGTAGCAGCTTGTAGCCGTGTACAGCAGAAA 189  
DB 126 CTCTCTCAGAGGCGCAGTGTAGTGTAGCAGCTTGTAGCCGTGTACAGCAGAAA 185  
QY 190 CTGAGCAGGCTCCAGGCTCTCATCTATGTGTATCCAGCAGGCGCATGCGCATGCCA 249  
DB 186 CTGAGCAGGCTCCAGGCTCTCATCTATGTGTATCCAGCAGGCGCATGCGCATGCCA 245  
QY 250 GACAGGTTCAAGGCGAGGCGGCTCCGAGAGAGACTTCACTCAACATCATAGTGAAG 309

Db 246 GAAGGTTGAGTGGAGTGGTCTGGGACAGACTTCACTTCACATCAGACAGACTGGAG 305

QY 310 CTTGAAGATTTTSCAGTGTATTACTGTACAGCAGTATGTAGTCTACCTCAGACACTCAG 369

Db 306 CTTGAAGATTTTSCAGTGTATTACTGTACAGCAGTATGTAGTCTACCTCAG-----AG 359

QY 370 ATACCTTTGGGGGAGGACCAAGGTGGAGATCAACGAACTGTGGCTGCACATCTGTC 429

Db 360 GTACCTTTGGGGGAGGACCAAGGTGGAGATTAACGAACTGTGGCTGCACATCTGTC 419

QY 430 T 430

Db 420 T 420

RESULT 9  
 BI759245 745 bp mRNA linear EST 25-SEP-2001  
 LOCUS 603042678F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5183010 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI759245  
 VERSION BI759245.1 GI:15750823  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
 1 (bases 1 to 745)  
 TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgsab@femail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHAM11456 row: 1 column: 19  
 High quality sequence stop: 724.  
 Location/Qualifiers  
 1..745  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5183010"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_116"  
 /notes="Organ: pooled colon, kidney, stomach; Vector:  
 pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA  
 source anonymous pool of 3 colons, age 26 yo male, 49 yo  
 female, 71 yo male colon; 46 yo male kidney, and pool of 2  
 stomachs; 62 yo male and 70 yo female. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.4 Kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 023. Note: this is a NIH\_MGC library."

## ORIGIN

Query Match 33.6%; Score 308; DB 4; Length 745;  
 Best Local Similarity 85.8%; Pred. No. 2e-74;  
 Matches 357; Conservative 0; Mismatches 50; Indels 9; Gaps 1;

QY 15 AACCGCTATCGGATCGAGTGCAGTGGTGGTTCGATCCGTCGCGAGCCGATAT 74

Db 21 AAACCCGAGGAGGCTTCTCTCTCTCTCTGCTACTGCTGCCAGATACACCGAGAAA 80

QY 75 TGTGTGAGCAGAGTCTCAGAGCACCTGTCTTGTCTCCAGGGGAAAGACACCTCTC 134

Db 81 TGTGTGAGCAGAGTCTCAGAGCACCTGTCTTGTCTCTCAGGGGAAAGACACCTCTC 140

QY 135 CTGAGGGGCAAGTCAAGATGTTAGTACAGCTACTTACCTGTGTACAGCAGAAACCTGG 194

Db 141 CTGAGGGGCAAGTCAAGATGTTAGTACAGCTACTTACCTGTGTACAGCAGAAACCTGG 200

QY 195 CCAAGCTCCCAAGGCTCCATCTATGTGATCCACAGGGGCACTGGCATGCCAGAG 254

Db 201 CCAAGCTCCCAAGGCTCCATCTATGTGATCCACAGGGGCACTGGCATGCCAGAG 260

QY 255 GTTCAGTGGCAGTGGGTCCGGACAGACTTCACCTACCATCAGTACAGTGAAGCTTGA 314

Db 261 GTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCTACCATCAGCAGACTGGAGCCGA 320

QY 315 AGATTTTGCAGTGTATTACTGTACAGCAGTATGTAGTCTCAGACCTCAGATCAG 374

Db 321 AGATTTTGCAGTGTATTACTGTCAACAGTATATGTTCT-----CAGCTCGGCTCAG 371

QY 375 TTTTCGGGAGGAGGACCAAGGTGGAGATCAACGAACTGTGGCTGCACCATCTGTCT 430

Db 372 TTTTCGGGAGGAGGACCAAGGTGGAGATCAACGAACTGTGGCTGCACCATCTGTCT 427

RESULT 10  
 AV647117 433 bp mRNA linear EST 15-JAN-2002  
 LOCUS AV647117 GLC Homo sapiens cDNA clone GLCAUH04 3', mRNA sequence.  
 DEFINITION AV647117  
 ACCESSION AV647117  
 VERSION AV647117.1 GI:9868131  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 433)  
 TITLES Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 AUTHORS Xiao,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,  
 Xie,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,  
 Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,  
 Hu,G., Gu,J., Chen,Z. and Han,Z.  
 Insight into hepatocellular carcinogenesis at transcriptome level  
 by comparing gene expression profiles of hepatocellular carcinoma  
 with those of corresponding noncancerous liver  
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)  
 JOURNAL 21625106  
 MEDLINE  
 PUBMED 11752456

## COMMENT

Contact: Zeguana Han  
 Chinese National Human Genome Center at Shanghai  
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
 201203, P. R. China  
 Tel: 86-21-50801919(ex.45)  
 Fax: 86-21-50801922  
 Email: hanzg@chgc.sh.cn  
 This clone is available at CHGC in Shanghai.  
 Location/Qualifiers  
 1..433  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="GLCAUH04"  
 /tissue type="corresponding non cancerous liver tissue"  
 /dev stage="Adult"  
 /lab\_host="SOIR"  
 /clone\_lib="GLC"  
 /note="Vector: pBluescript sk(-), Site\_1: EcoRI; Site\_2:  
 XhoI"

## FEATURES

source

## ORIGIN

Query Match 33.5%; Score 307 8; DB 1; Length 433;  
 Best Local Similarity 93.4%; Pred. No. 2e-74;  
 Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

QY 70 GATATTTGTGAGCAGTCTCAGAGCACCTGTCTTGTCTCCAGGGGAAAGACCAACC 129

Db 83 GAAATGTGTGACGAGCTCTCCAGGAGCGCTGTCTTTGTCTTCAGGGGAAAAGGCCACC 142

Qy 130 CTCTCTGCAAGGCGCAGTCAAGATGTTAGTACAGCTTACTTGGTACCGAGAGAA 189

Db 143 CTCTCTGCAAGGCGCAGTCAAGATGTTAGTACAGCTTACTTGGTACCGAGAGAA 202

Qy 190 CCGGCGCAGGCTCCCGAGGCTCCCATCTTATGTCATCCAGGCGCCTGGCAGTCCA 249

Db 203 CTGGCGCAGGCTCCCGAGGCTCCCATCTTATGTCATCCAGGCGCCTGGCAGTCCA 262

Qy 250 GACAGTTGAGTGGCAGTGGGTCCGGGAGACATTCATCTCCATCAGTACAGTGGAG 309

Db 263 GACAGTTGAGTGGCAGTGGGTCCGGGAGACATTCATCTCCATCAGTACAGTGGAG 322

Qy 310 CCTGAAGATTTTGCAGTGATTAATCTGTCAAGCAGTATGTAAGTCACTTACAGACCTGAG 369

Db 323 CCTGAAGATTTTGCAGTGATTAATCTGTCAAGCAGTATGTAAGTCACTTACAGACCTGAG 371

Qy 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGAGTGGCTGACCATCTGTC 429

Db 372 -TCACCTTGGCGGAGGAGCAAGGTGAGATCAAGAGTGGCTGACCATCTGTC 430

Qy 430 T 430

Db 431 T 431

RESULT 11

AV647111 440 bp mRNA linear EST 15-JAN-2002

LOCUS AV647111 GUC Homo sapiens cDNA clone GLCAUG10 3', mRNA sequence.

DEFINITION AV647111

ACCESSION AV647111 GI:9868125

VERSION AV647111.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 440)

AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Hu,G., Gu,J., Chen,Z. and Han,Z.

TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

MEDLINE 21652106

PUBMED 11752456

COMMENT Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China  
Tel: 86-21-50801919 (ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.

FEATURES

source 1..440

location/Qualifiers

1..440

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="GLCAUG10"

/tissue\_type="corresponding non cancerous liver tissue"

/dev\_stage="Adult"

/lab\_host="SOLR"

/clone\_lib="GLC"

/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN

Query Match 33.5%; Score 307.8; DB 1; Length 440;

Best Local Similarity 93.4%; Pred. No. 2e-74;

Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

Qy 70 GAAATGTGTGACGAGCTCTCCAGGAGCGCTGTCTTTGTCTTCAGGGGAAAAGGCCACC 129

Db 91 GAAATGTGTGACGAGCTCTCCAGGAGCGCTGTCTTTGTCTTCAGGGGAAAAGGCCACC 150

Qy 130 CTCTCTGCAAGGCGCAGTCAAGATGTTAGTACAGCTTACTTGGTACCGAGAGAA 189

Db 151 CTCTCTGCAAGGCGCAGTCAAGATGTTAGTACAGCTTACTTGGTACCGAGAGAA 210

Qy 190 CCGGCGCAGGCTCCCGAGGCTCCCATCTTATGTCATCCAGGCGCCTGGCAGTCCA 249

Db 211 CTGGCGCAGGCTCCCGAGGCTCCCATCTTATGTCATCCAGGCGCCTGGCAGTCCA 270

Qy 250 GACAGTTGAGTGGCAGTGGGTCCGGGAGACATTCATCTCCATCAGTACAGTGGAG 309

Db 271 GACAGTTGAGTGGCAGTGGGTCCGGGAGACATTCATCTCCATCAGTACAGTGGAG 330

Qy 310 CCTGAAGATTTTGCAGTGATTAATCTGTCAAGCAGTATGTAAGTCACTTACAGACCTGAG 369

Db 331 CCTGAAGATTTTGCAGTGATTAATCTGTCAAGCAGTATGTAAGTCACTTACAGACCTGAG 379

Qy 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGAGTGGCTGACCATCTGTC 429

Db 380 -TCACCTTGGCGGAGGAGCAAGGTGAGATCAAGAGTGGCTGACCATCTGTC 438

Qy 430 T 430

Db 439 T 439

RESULT 12

AW405787 504 bp mRNA linear EST 16-FEB-2000

LOCUS AW405787

DEFINITION UI-HF-BL0-abp-e-02-0-UI.r1 NIH-MGC\_37 Homo sapiens cDNA clone IMAGE:3057482 5', mRNA sequence.

ACCESSION AW405787

VERSION AW405787.1 GI:6924844

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 504)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE NIH-MGC

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
cDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: www.bio.lnl.gov/bbrp/image/image.html  
Seq primer: M3 Forward.

FEATURES

source 1..504

location/Qualifiers

1..504

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3057482"

/tissue\_type="lymph"

/cell\_type="germinal center B cells"

/cell\_line="MGC85"

/lab\_host="DH10B (LTI)"

/clone\_lib="NIH-MGC\_37"

/note="Vector: pRT3-Pac; Site\_1: NotI; Site\_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima

ORIGIN Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

Query Match 33.5%; Score 307.8; DB 2; Length 504;  
Best Local Similarity 93.4%; Pred. No. 2.1e-74;  
Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

QY 70 GATATTGTGTGACGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGGCCACC 129  
DB 74 GAAATTGTGTGACGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGGCCACC 133  
QY 130 CTCTCCGACGGCCAGTCAAGTGTAGTACGAGTCTAGCTGTAGTACGAGGAAA 189  
DB 134 CTCTCTGACGGCCAGTCAAGTGTAGTACGAGTCTAGCTGTAGTACGAGGAAA 193  
QY 190 CTGCGCCAGGCTCCAGGCTCTCATCTATGTATGTGATCCAGGGCCACTGTGATGCA 249  
DB 194 CTGCGCCAGGCTCCAGGCTCTCATCTATGTATGTGATCCAGGGCCACTGTGATGCA 253  
QY 250 GACAGTTGATGAGTGTGGTCCGGGACAGACTTCACTCTCACTAGTATGATGAG 309  
DB 254 GACAGTTGATGAGTGTGGTCCGGGACAGACTTCACTCTCACTAGTATGAGT 313  
QY 310 CCTGAAGATTTTGACGTATTTACTGTAGCAGTATGTAGTCACTGACAGACCTGAG 369  
DB 314 CCGAAGATTTTGACGTATTTACTGTAGCAGTATGTAGTCACTGAGTCACTGAG 364  
QY 370 ATCACTTTGCGCGGAGGACCAAGGTGAGATCAAAAGAACTGTGCTGACCATGTGC 429  
DB 365 ---ACGTCGGCCAAAGGACCAAGGTGAGATCAAAAGAACTGTGCTGACCATGTGC 421  
QY 430 T 430  
DB 422 T 422

RESULT 13  
BG686748 734 bp mRNA linear EST 01-MAY-2001  
LOCUS 602650717F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4763021 5',  
DEFINITION mRNA sequence.  
ACCESSION BG686748  
VERSION BG686748.1 GI:13918145  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: c9abbs-r@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCML618 row: a column: 06  
High quality sequence stop: 709.  
Location/Qualifiers

FEATURES  
source 1..734  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4763021"  
/issue\_type="Primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_48"  
/note="Organ: B-cells; Vector: pOTB7; Site\_1: XhoI;

Site\_2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 33.5%; Score 307.8; DB 4; Length 734;  
Best Local Similarity 93.4%; Pred. No. 2.3e-74;  
Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

QY 70 GATATTGTGTGACGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGGCCACC 129  
DB 67 GAAATTGTGTGACGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGGCCACC 126  
QY 130 CTCTCCGACGGCCAGTCAAGTGTAGTACGAGTCTAGCTGTAGTACGAGGAAA 189  
DB 127 CTCTCTGACGGCCAGTCAAGTGTAGTACGAGTCTAGCTGTAGTACGAGGAAA 186  
QY 190 CTGCGCCAGGCTCCAGGCTCTCATCTATGTATGTGATCCAGGGCCACTGTGATGCA 249  
DB 187 CTGCGCCAGGCTCCAGGCTCTCATCTATGTATGTGATCCAGGGCCACTGTGATGCA 246  
QY 250 GACAGTTGATGAGTGTGGTCCGGGACAGACTTCACTCTCACTAGTATGATGAG 309  
DB 247 GACAGTTGATGAGTGTGGTCCGGGACAGACTTCACTCTCACTAGTATGAGT 306  
QY 310 CCTGAAGATTTTGACGTATTTACTGTAGCAGTATGTAGTCACTGACAGACCTGAG 369  
DB 307 CCGAAGATTTTGACGTATTTACTGTAGCAGTATGTAGTCACTGAGTCACTGAG 357  
QY 370 ATCACTTTGCGCGGAGGACCAAGGTGAGATCAAAAGAACTGTGCTGACCATGTGC 429  
DB 358 ---ACGTCGGCCAAAGGACCAAGGTGAGATCAAAAGAACTGTGCTGACCATGTGC 414  
QY 430 T 430  
DB 415 T 415

RESULT 14  
AV646708 793 bp mRNA linear EST 15-JAN-2002  
LOCUS AV646708 GLC Homo sapiens cDNA clone GICAOB01 3', mRNA sequence.  
DEFINITION AV646708  
ACCESSION AV646708  
VERSION AV646708.1 GI:9867722  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: c9abbs-r@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCML618 row: a column: 06  
High quality sequence stop: 709.  
Location/Qualifiers

FEATURES  
source 1..734  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4763021"  
/issue\_type="Primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_48"  
/note="Organ: B-cells; Vector: pOTB7; Site\_1: XhoI;

CONTACT: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919 (ex. 45)  
Fax: 86-21-50801922  
Email: hanzg@chc.sh.cn  
This clone is available at CHGC in Shanghai.

FEATURES  
source

Location/Qualifiers  
1. 793  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="GLCA0E01"  
/tissue\_type="corresponding non cancerous liver tissue"  
/dev\_stage="Adult"  
/lab\_host="SOLR"  
/clone\_11b="GLC"  
/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

## ORIGIN

Query Match 33.5%; Score 307.8; DB 1; Length 793;  
Best Local Similarity 93.4%; Pred. No. 2.3e-74;  
Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

70 GATATTGTTGACGAGCTCCAGGACCCCTGTTCTTCCTCCAGGGGAAAGCCACC 129  
57 GAAATTGTTGACGAGCTCCAGGACCCCTGTTCTTCCTCCAGGGGAAAGCCACC 116  
130 CTCTCTGAGGGGCGAGTCAAGTGTAGTACAGCTTACCTGTATCCAGAGAAA 189  
117 CTCTCTGAGGGGCGAGTCAAGTGTAGTACAGCTTACCTGTATCCAGAGAAA 176  
190 CTGAGCGAGGCTCCAGGCTCTCATCTATGTTGATCCAGGAGGCACTGGCATGCCA 249  
177 CTGAGCGAGGCTCCAGGCTCTCATCTATGTTGATCCAGGAGGCACTGGCATGCCA 236  
250 GACAGGTTCAAGTGGAGTGGGTCGGGAGAGACTTCACTCTACCTACAGTACGTGGAG 309  
237 GACAGGTTCAAGTGGAGTGGGTCGGGAGAGACTTCACTCTACCTACAGTACGTGGAG 296  
310 CCTGAAGATTTTGACAGTGTATTAAGTCAAGTGTAGTCACTCAAGACCTGAC 369  
297 CCTGAAGATTTTGACAGTGTATTAAGTCAAGTGTAGTCACTCAAGACCTGAC 345  
370 ATCACTTTGGGCGAGGAGCAAGGTGAGATCAAGCAAGTGTGGCTGACCATCTGTC 429  
346 -TCACCTTTGGGCGAGGAGCAAGGTGAGATCAAGCAAGTGTGGCTGACCATCTGTC 404  
430 T 430  
405 T 405

RESULT 15  
BO706634 926 bp mRNA linear EST 16-JUL-2002  
LOCUS BO706634  
DEFINITION AGENCOURT\_7975592 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6215094  
5', mRNA sequence.  
ACCESSION BO706634  
VERSION BO706634.1 GI:21845533  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 926)  
NIH-MGC <http://mgs.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ULNL at:  
<http://image.llnl.gov>  
Plate: L1CM2383 row: h column: 07

## High quality sequence stop: 536.

FEATURES  
source

Location/Qualifiers  
1. 926  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6215094"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_11b="NIH MGC 113"  
/note="Organ: spleen; Vector: pOT87; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

## ORIGIN

Query Match 33.5%; Score 307.8; DB 5; Length 926;  
Best Local Similarity 93.4%; Pred. No. 2.4e-74;  
Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

70 GATATTGTTGACGAGCTCCAGGACCCCTGTTCTTCCTCCAGGGGAAAGCCACC 129  
67 GAAATTGTTGACGAGCTCCAGGACCCCTGTTCTTCCTCCAGGGGAAAGCCACC 126  
130 CTCTCTGAGGGGCGAGTCAAGTGTAGTACAGCTTACCTGTATCCAGAGAAA 189  
127 CTCTCTGAGGGGCGAGTCAAGTGTAGTACAGCTTACCTGTATCCAGAGAAA 186  
190 CTGAGCGAGGCTCCAGGCTCTCATCTATGTTGATCCAGGAGGCACTGGCATGCCA 249  
187 CTGAGCGAGGCTCCAGGCTCTCATCTATGTTGATCCAGGAGGCACTGGCATGCCA 246  
250 GACAGGTTCAAGTGGAGTGGGTCGGGAGAGACTTCACTCTACCTACAGTACGTGGAG 309  
247 GACAGGTTCAAGTGGAGTGGGTCGGGAGAGACTTCACTCTACCTACAGTACGTGGAG 306  
310 CCTGAAGATTTTGACAGTGTATTAAGTCAAGTGTAGTCACTCAAGACCTGAC 369  
307 CCTGAAGATTTTGACAGTGTATTAAGTCAAGTGTAGTCACTCAAGACCTGAC 354  
370 ATCACTTTGGGCGAGGAGCAAGGTGAGATCAAGCAAGTGTGGCTGACCATCTGTC 429  
355 CTCACTTTGGGCGAGGAGCAAGGTGAGATCAAGCAAGTGTGGCTGACCATCTGTC 414  
430 T 430  
415 T 415

Search completed: February 18, 2005, 08:24:27  
Job time : 3738 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 04:06:26 ; Search time 4372 Seconds  
(without alignments)

10174.265 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 918  
Sequence: 1 GAATTCATGAAAAAACCAGCC.....ATCACCATTAGTGAAGCTT 918

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 2422767955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ha:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sbs:\*  
12: gb\_by:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	918	100.0	918	6	AR139128 Sequence
2	916.4	99.8	918	6	AR139129 Sequence
3	799.6	87.1	867	6	AR139130 Sequence
4	798	86.9	867	6	AR139131 Sequence
5	463.8	50.5	801	12	AF027160 Synthetic
6	445	48.5	1630	6	BD222938 Heteromycin
7	445	48.5	1630	6	BD222939 Heteromycin
8	445	48.5	1630	6	AX023365 Sequence
9	445	48.5	1630	6	AX023367 Sequence
10	414.4	45.1	867	12	AF416910 Synthetic
11	380.8	40.3	861	12	AF416909 Synthetic
12	369.6	40.3	861	12	AF416909 Synthetic
13	361	39.3	450	6	AR139120 Sequence
14	359.4	39.2	450	6	AR139121 Sequence
15	358.4	39.0	790	10	MMVJ5051 Mus muscu
16	352	38.3	790	10	MMVJ24FRG
17	348.4	37.7	762	6	AX601792 Sequence
18	346.2	37.6	864	12	XXU34924 Synthetic r
19	345.2	37.6	780	12	SYNN19886CF

20	345.2	37.6	783	6	AR198737 Sequence
21	343.6	37.4	786	6	AX601794 Sequence
22	343.6	37.4	1848	6	173512 Sequence 15
23	343.6	37.4	1848	12	U06943 Synthetic c
24	342.8	37.3	771	6	AX601793 Sequence
25	342.8	36.4	1953	6	AX797328 Sequence
26	344.6	36.4	1956	6	AX797327 Sequence
27	329	35.8	786	6	AX601796 Sequence
28	327.6	35.7	765	12	AF377321 Synthetic
29	326	35.5	888	6	AX055802 Sequence
30	324.4	35.3	543	6	AR139118 Sequence
31	324.4	35.3	543	6	AR139119 Sequence
32	321.2	35.0	811	9	AB064067 Homo sapi
33	321	35.0	735	6	E13598 DNA encodin
34	319.8	34.8	1413	6	BD185289 Uses of a
35	319.8	34.8	1413	6	BD273725 Human mon
36	319.8	34.8	1413	6	AR454402 Sequence
37	319.8	34.8	1413	6	AX616568 Sequence
38	318.4	34.7	4691	6	AR370701 Sequence
39	318.4	34.7	6166	6	AR370702 Sequence
40	315	34.3	753	6	I08679 Sequence 12
41	314.8	34.3	833	9	AB064110 Homo sapi
42	314.6	34.3	378	9	AJ555261 Homo sapi
43	314.2	34.2	376	9	AY640472 Homo sapi
44	314.2	34.2	376	9	AY640535 Homo sapi
45	314.2	34.2	518	9	AY393155 Homo sapi

#### ALIGNMENTS

RESULT 1	AR139128	918 bp	DNA	linear	PAT 16-JUN-2001
LOCUS	Sequence 13 from patent US 6207153.				
DEFINITION	AR139128				
ACCESSION	AR139128.1	GI:14481624			
VERSION					
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 918)				
AUTHORS	Dan, M.D., Maiti, P.K. and Kaplan, H.A.				
TITLE	Antigen binding fragments that specifically detect cancer cells, nucleotides encoding the fragments, and use thereof for the prophylaxis and detection of cancers				
JOURNAL	Patent: US 6207153-A 13 27-MAR-2001;				
FEATURES	location/Qualifiers				
source	1..918				
ORIGIN	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	100.0%; Score 918; DB 6; Length 918;				
Best Local Similarity	100.0%; Pred. No. 5.8e-247;				
Matches	918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 GAATTCATGAAAAAACCAGCTATCGCATCGCATGTCAGTTCGCTGCTTCCGTA	60			
DB	1 GAATTCATGAAAAAACCAGCTATCGCATCGCATGTCAGTTCGCTGCTTCCGTA	60			
QY	61 GCGCAGCCGATATGTTGACGAGCTCTCAGGACCCCTGCTTTGTTCTCCAGGGCA	120			
DB	61 GCGCAGCCGATATGTTGACGAGCTCTCAGGACCCCTGCTTTGTTCTCCAGGGCA	120			
QY	121 AGAGCACCTCTCTCGAGGGCCAGTCAAGTGTAGAGCAGCTACTTACCTGTAC	180			
DB	121 AGAGCACCTCTCTCGAGGGCCAGTCAAGTGTAGAGCAGCTACTTACCTGTAC	180			
QY	181 CAGCAGAAACCTGCGCAGCTCCAGGCTCTCATCTATGTGTCATCCAGGCGCACT	240			
DB	181 CAGCAGAAACCTGCGCAGCTCCAGGCTCTCATCTATGTGTCATCCAGGCGCACT	240			

QY 241 GGCATGCCAGACAGGTTCACTGAGTGGGTCCGGACAGACTTCACTCTCAACCATCACT 300  
|  
|  
|  
Db 241 GGCATGCCAGACAGGTTCACTGAGTGGGTCCGGACAGACTTCACTCTCAACCATCACT 300  
|  
|  
|  
QY 301 AGACTGGAGCTGAAGATTTTTCAGTGTATTACTGTCAAGATATGATGATCACTCACTGAG 360  
|  
|  
|  
Db 301 AGACTGGAGCTGAAGATTTTTCAGTGTATTACTGTCAAGATATGATGATCACTCACTGAG 360  
|  
|  
|  
QY 361 ACACCTCAAGATCACTTTCCGCGAGGAGACCAAGGTGAGATCAACGAACTGTGGCTGCA 420  
|  
|  
|  
Db 361 ACACCTCAAGATCACTTTCCGCGAGGAGACCAAGGTGAGATCAACGAACTGTGGCTGCA 420  
|  
|  
|  
QY 421 CCATCTGTCTCTGCGCGGTGCGGTCCGAGAGTGTGATCAAGTGAAGTGGCTCCGAG 480  
|  
|  
|  
Db 421 CCATCTGTCTCTGCGCGGTGCGGTCCGAGAGTGTGATCAAGTGAAGTGGCTCCGAG 480  
|  
|  
|  
QY 481 GTGCACTGGTGAAGTCTGGGGGAGGCGTGTCTCAAGCTGGAGAGTCCCTGAGACTCTCC 540  
|  
|  
|  
Db 481 GTGCACTGGTGAAGTCTGGGGGAGGCGTGTCTCAAGCTGGAGAGTCCCTGAGACTCTCC 540  
|  
|  
|  
QY 541 TGTGACGCTCTGAGATTTCCCTTTCAAGAGCTTTGCTATGCACTGGGTCCGCAAGCTCTA 600  
|  
|  
|  
Db 541 TGTGACGCTCTGAGATTTCCCTTTCAAGAGCTTTGCTATGCACTGGGTCCGCAAGCTCTA 600  
|  
|  
|  
QY 601 GGCAGAGGGCTGAGAGTGGGTGAGATTAATATCAATATGAGAGCACTAAATATCAACGA 660  
|  
|  
|  
Db 601 GGCAGAGGGCTGAGAGTGGGTGAGATTAATATCAATATGAGAGCACTAAATATCAACGA 660  
|  
|  
|  
QY 661 GACTCCGTGAAGGGCCGATTTCAACATCTCCAGAGACATTTCCAAAGAACCGGTATCTA 720  
|  
|  
|  
Db 661 GACTCCGTGAAGGGCCGATTTCAACATCTCCAGAGACATTTCCAAAGAACCGGTATCTA 720  
|  
|  
|  
QY 721 AAAATGAACAGCTTGAGAACTGAGACACGCGTCTTATTACTGTGCGAGAGATCAAGAC 780  
|  
|  
|  
Db 721 AAAATGAACAGCTTGAGAACTGAGACACGCGTCTTATTACTGTGCGAGAGATCAAGAC 780  
|  
|  
|  
QY 781 CTGTTGGGTGACTATACCACTACAGGTTTGGAGCGTCCGGGGCAAAAGGACACAGGTC 840  
|  
|  
|  
Db 781 CTGTTGGGTGACTATACCACTACAGGTTTGGAGCGTCCGGGGCAAAAGGACACAGGTC 840  
|  
|  
|  
QY 841 ACCGTCTCTCAGAGATCCGAACAAAACATGATCAGGAAAGATCTGAACCATCAACAT 900  
|  
|  
|  
Db 841 ACCGTCTCTCAGAGATCCGAACAAAACATGATCAGGAAAGATCTGAACCATCAACAT 900  
|  
|  
|  
QY 901 CACCATTAAGTGAAGCTT 918  
|  
|  
|  
Db 901 CACCATTAAGTGAAGCTT 918  
|  
|  
|

RESULT 2  
ARI39129/c 918 bp DNA linear PAT 16-JUN-2001  
LOCUS ARI39129  
DEFINITION Sequence 15 from patent US 6207153.  
ACCESSION ARI39129  
VERSION ARI39129.1 GI:14481625  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 918)  
AUTHORS Dan, M.D., Mafti, P.K. and Kaplan, H.A.  
TITLE Antigen binding fragments that specifically detect cancer cells,  
nucleotides encoding the fragments, and use thereof for the  
prophylaxis and detection of cancers  
JOURNAL Patent: US 6207153-A 15 27-MAR-2001;  
FEATURES Location/Qualifiers  
1..918  
source /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 99.8%; Score 916.4; DB 6; Length 918;  
Best Local Similarity 99.9%; Pred. No. 1.6e-246;

Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GAATTCATGAAAAAACCGCTATGCGATGCGAGTTGCACTGGCTGTTGGCTAACGTT 60  
|  
|  
|  
Db 918 GAATTCATGAAAAAACCGCTATGCGATGCGAGTTGCACTGGCTGTTGGCTAACGTT 859  
|  
|  
|  
QY 61 GGGAGGCGCGATATTGTGTTTGAACCGAGTCTCAAGGCAACCGTCTTGTGTCACAGGGAA 120  
|  
|  
|  
Db 61 GGGAGGCGCGATATTGTGTTTGAACCGAGTCTCAAGGCAACCGTCTTGTGTCACAGGGAA 120  
|  
|  
|  
QY 61 GGGAGGCGCGATATTGTGTTTGAACCGAGTCTCAAGGCAACCGTCTTGTGTCACAGGGAA 120  
|  
|  
|  
Db 61 GGGAGGCGCGATATTGTGTTTGAACCGAGTCTCAAGGCAACCGTCTTGTGTCACAGGGAA 120  
|  
|  
|  
QY 121 AGAGCAACCTCTCTCTGAGGCGCAGTCAAGTGTATGAGAGCTTATGAGCTGTATC 180  
|  
|  
|  
Db 121 AGAGCAACCTCTCTCTGAGGCGCAGTCAAGTGTATGAGAGCTTATGAGCTGTATC 180  
|  
|  
|  
QY 181 CAGCAAAAACCTGGCCAGGCTTCCAGGCTCTCATCTATGTTGTCATCCAGAGGCTACT 240  
|  
|  
|  
Db 181 CAGCAAAAACCTGGCCAGGCTTCCAGGCTCTCATCTATGTTGTCATCCAGAGGCTACT 240  
|  
|  
|  
QY 241 GGCATGCCAGACAGGTTCACTGAGTGGGTCCGGACAGACTTCACTCAACCATCACT 300  
|  
|  
|  
Db 241 GGCATGCCAGACAGGTTCACTGAGTGGGTCCGGACAGACTTCACTCAACCATCACT 300  
|  
|  
|  
QY 301 AGACTGGAGCTGAAGATTTTTCAGTGTATTACTGTCAAGATATGATGATCACTCACTGAG 360  
|  
|  
|  
Db 301 AGACTGGAGCTGAAGATTTTTCAGTGTATTACTGTCAAGATATGATGATCACTCACTGAG 360  
|  
|  
|  
QY 361 ACACCTCAAGATCACTTTCCGCGAGGAGACCAAGGTGAGATCAACGAACTGTGGCTGCA 420  
|  
|  
|  
Db 361 ACACCTCAAGATCACTTTCCGCGAGGAGACCAAGGTGAGATCAACGAACTGTGGCTGCA 420  
|  
|  
|  
QY 421 CCATCTGTCTCTGCGCGGTGCGGTCCGAGAGTGTGATCAAGTGAAGTGGCTCCGAG 480  
|  
|  
|  
Db 421 CCATCTGTCTCTGCGCGGTGCGGTCCGAGAGTGTGATCAAGTGAAGTGGCTCCGAG 480  
|  
|  
|  
QY 481 GTGCACTGGTGAAGTCTGGGGGAGGCGTGTCTCAAGCTGGAGAGTCCCTGAGACTCTCC 540  
|  
|  
|  
Db 481 GTGCACTGGTGAAGTCTGGGGGAGGCGTGTCTCAAGCTGGAGAGTCCCTGAGACTCTCC 540  
|  
|  
|  
QY 541 TGTGACGCTCTGAGATTTCCCTTTCAAGAGCTTTGCTATGCACTGGGTCCGCAAGCTCTA 600  
|  
|  
|  
Db 541 TGTGACGCTCTGAGATTTCCCTTTCAAGAGCTTTGCTATGCACTGGGTCCGCAAGCTCTA 600  
|  
|  
|  
QY 601 GGCAGAGGGCTGAGAGTGGGTGAGATTAATATCAATATGAGAGCACTAAATATCAACGA 660  
|  
|  
|  
Db 601 GGCAGAGGGCTGAGAGTGGGTGAGATTAATATCAATATGAGAGCACTAAATATCAACGA 660  
|  
|  
|  
QY 661 GACTCCGTGAAGGGCCGATTTCAACATCTCCAGAGACATTTCCAAAGAACCGGTATCTA 720  
|  
|  
|  
Db 661 GACTCCGTGAAGGGCCGATTTCAACATCTCCAGAGACATTTCCAAAGAACCGGTATCTA 720  
|  
|  
|  
QY 721 AAAATGAACAGCTTGAGAACTGAGACACGCGTCTTATTACTGTGCGAGAGATCAAGAC 780  
|  
|  
|  
Db 721 AAAATGAACAGCTTGAGAACTGAGACACGCGTCTTATTACTGTGCGAGAGATCAAGAC 780  
|  
|  
|  
QY 781 CTGTTGGGTGACTATACCACTACAGGTTTGGAGCGTCCGGGGCAAAAGGACACAGGTC 840  
|  
|  
|  
Db 781 CTGTTGGGTGACTATACCACTACAGGTTTGGAGCGTCCGGGGCAAAAGGACACAGGTC 840  
|  
|  
|  
QY 841 ACCGTCTCTCAGAGATCCGAACAAAACATGATCAGGAAAGATCTGAACCATCAACAT 900  
|  
|  
|  
Db 841 ACCGTCTCTCAGAGATCCGAACAAAACATGATCAGGAAAGATCTGAACCATCAACAT 900  
|  
|  
|  
QY 901 CACCATTAAGTGAAGCTT 918  
|  
|  
|  
Db 901 CACCATTAAGTGAAGCTT 918  
|  
|  
|

RESULT 3  
ARI39130 867 bp DNA linear PAT 16-JUN-2001  
LOCUS ARI39130  
DEFINITION Sequence 16 from patent US 6207153.  
ACCESSION ARI39130  
VERSION ARI39130.1 GI:14481626



KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 867)  
AUTHORS Dan, M.D., Maiti, P.K. and Kaplan, H.A.  
TITLE Antigen binding fragments that specifically detect cancer cells,  
nucleotides encoding the fragments, and use thereof for the  
prophylaxis and detection of cancers  
JOURNAL Patent: US 6207153-A 16 27-MAR-2001;  
FEATURES Location/Qualifiers  
source 1..867  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 87.1%; Score 799.6; DB 6; Length 867;  
Best Local Similarity 94.0%; Pred. No. 1.2e-213;  
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

QY 1 GAATTCATGAAAAAACCCTATCCGATCGCATGTCAGTGGCTGTTGCTACCGTT 60  
DB 1 GAATTCATGAAAAAACCCTATCCGATCGCATGTCAGTGGCTGTTGCTACCGTT 60  
QY 61 GCGCAGGCGCATATGTGTGAGCGAGTCTCCAGGCACTTCTTGTCTCCAGGGAA 120  
DB 61 GCGCAGGCGCATATGTGTGAGCGAGTCTCCAGGCACTTCTTGTCTCCAGGGAA 120  
QY 121 AGAGCCACCTCTCTCTGAGGGCCAGTCCAGATGTTAGTAGGAGGCTTACCTGTAC 180  
DB 121 AGAGCCACCTCTCTCTGAGGGCCAGTCCAGATGTTAGTAGGAGGCTTACCTGTAC 180  
QY 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGGCACT 240  
DB 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGGCACT 240  
QY 241 GGCATGCCAGACAGGTTCACTGGGTCGGGACAGACTTCACTTCACTCACTCACT 300  
DB 241 GGCATGCCAGACAGGTTCACTGGGTCGGGACAGACTTCACTTCACTCACTCACT 300  
QY 301 AGACTGAGACCTGAGATTTTTCAGTGTATTACTGTACAGATATGATGATCACTCAG 360  
DB 301 AGACTGAGACCTGAGATTTTTCAGTGTATTACTGTACAGATATGATGATCACTCAG 360  
QY 361 ACACCTCAGATCACTTTTGGCGGAGGACCAAGGTGAGATCAAAAGATGTGCTGCA 420  
DB 361 ACACCTCAGATCACTTTTGGCGGAGGACCAAGGTGAGATCAAAAGATGTGCTGCA 420  
QY 421 CCATCTGTCTCTGGGCGGTGCGGTTCGGAGGTGATCAGGTGAGAGTGGCTCCAG 480  
DB 421 TC-----CGAGCAG 429  
QY 481 GTGAGCTGTGAGATCTGGGGGAGCGGTGTCAGCCTGGGAGGTCCTGAGATCTCC 540  
DB 481 GTGAGCTGTGAGATCTGGGGGAGCGGTGTCAGCCTGGGAGGTCCTGAGATCTCC 540  
QY 430 GTGAGCTGTGAGATCTGGGGGAGCGGTGTCAGCCTGGGAGGTCCTGAGATCTCC 489  
DB 430 GTGAGCTGTGAGATCTGGGGGAGCGGTGTCAGCCTGGGAGGTCCTGAGATCTCC 489  
QY 541 TGTGAGCCTCTGAGATTTCCCTTCAGAACTTTTGTATGACTGGGTCCGCGAGGCTCTA 600  
DB 490 TGTGAGCCTCTGAGATTTCCCTTCAGAACTTTTGTATGACTGGGTCCGCGAGGCTCTA 549  
QY 601 GGCAGAGGCTGTGAGATGGGTGAGCTTATATCATATGATGAAAGCATTAATACCTACGCA 660  
DB 550 GGCAGAGGCTGTGAGATGGGTGAGCTTATATCATATGATGAAAGCATTAATACCTACGCA 609  
QY 661 GACTCCGTGAAGGCGCATTCACATCTCCAGAGACATTTCCAGAAACCGGTGATCTA 720  
DB 610 GACTCCGTGAAGGCGCATTCACATCTCCAGAGACATTTCCAGAAACCGGTGATCTA 669  
QY 721 AAATGAACAGCTGAGAACTGAGGACACGCGTGTCTATTAATGTGTGAGAGATCAGAGC 780  
DB 670 AAATGAACAGCTGAGAACTGAGGACACGCGTGTCTATTAATGTGTGAGAGATCAGAGC 729  
QY 781 CTGTTGGGTGACTATGACCACTACGCGTTTGGACGTCCTGGGGCAAGGACACGCGTC 840

DB 730 CTGTTGGGTGACTATGACCACTACCTACGCGTTTGGACGTCCTGGGGCAAGGACACGCGTC 789  
QY 841 ACCGTCTCTCAGATCCGACCAAAACTGATCAGCAGAGAGATCTGAACCATCACTCAT 900  
DB 790 ACCGTCTCTCAGATCCGACCAAAACTGATCAGCAGAGAGATCTGAACCATCACTCAT 849  
QY 901 CACCATTTGTGAAAGCTT 918  
DB 850 CACCATTTGTGAAAGCTT 867

RESULT 4  
AR139131/c 867 bp DNA linear PAT 16-JUN-2001  
LOCUS AR139131  
DEFINITION Sequence 18 from patent US 6207153.  
ACCESSION AR139131  
VERSION AR139131.1 GI:14481627  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 867)  
AUTHORS Dan, M.D., Maiti, P.K. and Kaplan, H.A.  
TITLE Antigen binding fragments that specifically detect cancer cells,  
nucleotides encoding the fragments, and use thereof for the  
prophylaxis and detection of cancers  
JOURNAL Patent: US 6207153-A 16 27-MAR-2001;  
FEATURES Location/Qualifiers  
source 1..867  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 86.9%; Score 798; DB 6; Length 867;  
Best Local Similarity 93.9%; Pred. No. 3.4e-213;  
Matches 862; Conservative 0; Mismatches 5; Indels 51; Gaps 1;

QY 1 GAATTCATGAAAAAACCCTATCCGATCGCATGTCAGTGGCTGTTGCTACCGTT 60  
DB 867 GAATTCATGAAAAAACCCTATCCGATCGCATGTCAGTGGCTGTTGCTACCGTT 808  
QY 61 GCGCAGGCGCATATGTGTGAGCGAGTCTCCAGGCACTTCTTGTCTCCAGGGAA 120  
DB 807 GCGCAGGCGCATATGTGTGAGCGAGTCTCCAGGCACTTCTTGTCTCCAGGGAA 748  
QY 121 AGAGCCACCTCTCTCTGAGGGCCAGTCCAGATGTTAGTAGGAGGCTTACCTGTGAC 180  
DB 747 AGAGCCACCTCTCTCTGAGGGCCAGTCCAGATGTTAGTAGGAGGCTTACCTGTGAC 688  
QY 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGGCACT 240  
DB 687 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGGCACT 628  
QY 241 GGCATGCCAGACAGGTTCACTGGGTCGGGACAGACTTCACTTCACTCACTCACT 300  
DB 627 GGCATGCCAGACAGGTTCACTGGGTCGGGACAGACTTCACTTCACTCACTCACT 300  
QY 301 AGACTGAGACCTGAGATTTTTCAGTGTATTACTGTACAGATATGATGATCACTCAG 360  
DB 567 AGACTGAGACCTGAGATTTTTCAGTGTATTACTGTACAGATATGATGATCACTCAG 508  
QY 361 ACACCTCAGATCACTTTTGGCGGAGGACCAAGGTGAGATCAAAAGATGTGCTGCA 420  
DB 507 ACACCTCAGATCACTTTTGGCGGAGGACCAAGGTGAGATCAAAAGATGTGCTGCA 448  
QY 421 CCATCTGTCTCTGGGCGGTGCGGTTCGGAGGTGATCAGGTGAGAGTGGCTCCAG 480  
DB 447 TC-----CGAGCAG 439  
QY 481 GTGAGCTGTGAGATCTGGGGGAGCGGTGTCAGCCTGGGAGGTCCTGAGATCTCC 540  
DB 438 GTGAGCTGTGAGATCTGGGGGAGCGGTGTCAGCCTGGGAGGTCCTGAGATCTCC 379

QY 541 TGTGACGCTCTGTGATTTCCCTTCAGAGAGCTTTGCTATGACATGGGTCCGCGAGCTCTA 600  
| | | | |  
Db 378 TGTGACGCTCTGTGATTTCCCTTCAGAGAGCTTTGCTATGACATGGGTCCGCGAGCTCTA 319  
| | | | |  
QY 601 GGCAGAGGGGCTGAGTGGGTGGAGTATATCATATGATGAGAGCACTAATACTAGCA 660  
| | | | |  
Db 318 GGCAGAGGGGCTGAGTGGGTGGAGTATATCATATGATGAGAGCACTAATACTAGCA 259  
| | | | |  
QY 661 GACTCCGTGAAGGGCCGATTTCACATCTCCAGAGACATTTCCAGAAACGCGTGTATCTA 720  
| | | | |  
Db 258 GACTCCGTGAAGGGCCGATTTCACATCTCCAGAGACATTTCCAGAAACGCGTGTATCTA 199  
| | | | |  
QY 721 AAATGAACAGCTGAGAGACATGAGAGACAGCGTCTCTATATCTGTGGAGAGATCAGAGC 780  
| | | | |  
Db 198 AAATGAACAGCTGAGAGACATGAGAGACAGCGTCTCTATATCTGTGGAGAGATCAGAGC 139  
| | | | |  
QY 781 CTGTGGGTGACTATGACCACTACTACGTTTGGACGTCGGGGCAAGAGGACCAAGGTC 840  
| | | | |  
Db 138 CTGTGGGTGACTATGACCACTACTACGTTTGGTCCTGTGGGGCAAGAGGACCAAGGTC 79  
| | | | |  
QY 841 ACCGTCTCTCAGAGATCCGAAACAAAATGATCAGAGAGAGATCTGAACATCAACAT 900  
| | | | |  
Db 78 ACCGTCTCTCAGAGATCCGAAACAAAATGATCAGAGAGAGATCTGAACATCAACAT 19  
| | | | |  
QY 901 CACCATTAAGTAAAGCTT 918  
| | | | |  
Db 18 CACCATTAAGTAAAGCTT 1

RESULT 5  
AF027160 801 bp mRNA linear SYN 06-FEB-2003  
LOCUS AF027160  
DEFINITION Synthetic construct single chain Fv fragment (TeJScFv07) mRNA,  
complete cds.  
VERSION AF027160.2 GI:23683339  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE  
1 (bases 1 to 801)  
Ohba,H., Kashima,K., Tomozawa,T. and Chiba,J.  
Molecular expression of human antibody and prediction of  
antigen-binding structure  
JOURNAL (in) PROCEEDINGS OF THE JAPANESE SOCIETY OF IMMUNOLOGY: 639;  
(1994)

REFERENCE  
2 (bases 1 to 801)  
Ohba,H., Kashima,K., Tomozawa,T. and Chiba,J.  
Direct Submission  
Submitted (29-SEP-1997) Department of Biological Sciences and  
Technology, Science University of Tokyo, 2641 Yamazaki, Noda, Chiba  
278, Japan  
3 (bases 1 to 801)  
Ohba,H., Kashima,K., Tomozawa,T. and Chiba,J.  
Direct Submission  
Submitted (10-OCT-2002) Department of Biological Sciences and  
Technology, Science University of Tokyo, 2641 Yamazaki, Noda, Chiba  
278, Japan

REMARK  
COMMENT Sequence update by submitter  
On Oct 10, 2002 this sequence version replaced gi:2623588.  
FEATURES  
location/Qualifiers  
1..801  
/organism="synthetic construct"  
/mol\_type="mRNA"  
/db\_xref="taxon:32630"  
/clone="TAPC6JCS"  
/note="TAPC6JCS hybridoma was made by fusing an EBV  
transformed B cell line, TAPC301-C14 with triple  
hybridoma, 6JCS; sequence based on human DNA"  
gene  
1..801  
/gene="TeJScFv07"  
1..801  
CDS

/gene="TeJScFv07"  
/note="specific to hepatitis B virus surface antigen"  
/codon\_start=1  
/transl\_table=11  
/product="single chain Fv fragment"  
/protein\_id="AAB86468.2"  
/db\_xref="gi:23683340"  
/translation="METPAQLLFLLMLPVSDTTGELVMTQSPATLSVSPGERATLS  
CRASQSVRSNLAHWQOKPQAPRLITVASTRAGIPARFSGSGSGTEFTLTISLQS  
EDFAVYVCOQYNWMPRTGQGTKEIKIKSGGGSGGGSGGGSLAEVQLVYESGGGV  
VQGRSLRLSCVAGSFTFSSYPMETWRQAPGKGLAEVAVSIYDGSYKYKVDKMKRLTI  
SRDSNKNTLYLIMNSLTFRBDTAIVYVCARTAFNAYDFMGQGTIVTVSS"  
1..801  
/gene="TeJScFv07"  
67..387  
/gene="TeJScFv07"  
/product="light chain Fv fragment"  
445..798  
/gene="TeJScFv07"  
/product="heavy chain Fv fragment"  
388..444  
/gene="TeJScFv07"  
/note="encodes flexible linker peptide"

ORIGIN

Query Match 50.5%; Score 463.8; DB 12; Length 801;  
Best Local Similarity 82.3%; Pred.No.3.9e-119;  
Matches 592; Conservative 0; Mismatches 97; Indels 30; Gaps 4;

QY 52 GCTACCGTGGCGAGGCGCATTTGTGTGACGAGTCTCCAGGACCCCTCTTGTGCT 111  
| | | | |  
Db 49 GTTTCAGATACCATCTGAGGAAATAGATGACGAGTCTCAGACCACTCTGTGTCT 108  
| | | | |  
QY 112 CCAGGGAAAGACCCCTCTCTGCAAGGCGCATGTCAGAGTGTAGTAGGAGCTACTTA 171  
| | | | |  
Db 109 CCAGGGAAAGACCCCTCTCTGCAAGGCGCATGTCAGAGTGTAGTAGGAGCA---ACTTA 165  
| | | | |  
QY 172 GCTCGTACCGACGAAACCTGGCGAGGCTCCAGGCTCCCTCATCTATGTGTCATCCACC 231  
| | | | |  
Db 166 GCTCGTACCGACGAAACCTGGCGAGGCTCCAGGCTCCCTCATCTATGTGTCATCCACC 225  
| | | | |  
QY 232 AGGCGCACTGCGATGCCGAGAGTTCAGTGGCAGTGGGTCCGGAGACAGACTTCACTTC 291  
| | | | |  
Db 226 AGGCGCACTGCTATCCAGCAGGTTCACTGGGTGTGGAGACAGACTTCACTTC 285  
| | | | |  
QY 292 ACCATCACTGACCTGAGAGCTGAAAGATTTTGCAGTGTATTACTGTCAAGCAATGTAGC 351  
| | | | |  
Db 286 ACCATCACTGACCTGAGAGCTGAAAGATTTTGCAGTGTATTACTGTCAAGCAATGTAGCA 345  
| | | | |  
QY 352 TCACCTCAGACACCTCAGATCACTTTGGCGGAGGACCAAGGTGAGATCAACGAACT 411  
| | | | |  
Db 346 TGTGTTCCG-----ACGTTCCGCCAAGGACCAAGGTGAGATCAACGAACT 393  
| | | | |  
QY 412 GTGCTGACCACTATGCTCTGCGGTGGCGGTCCGAGGTGGATCAGTGGAGGT 471  
| | | | |  
Db 394 GTGGAG-----GCGTTACAGGCGAGGTGGCTCTGGCGGTGGCGATGCTCG----- 442  
| | | | |  
QY 472 GGTCTCCAGAGTCTGCTGTGAGTCTGGGGGAGGCGGTGTCACGCTGGGAGGTCCCTG 531  
| | | | |  
Db 443 ----AGCAGGTGCGAGCTGTGGAGTCTGGGGGAGGCGGTGTCACGCTGGGAGGTCCCTG 498  
| | | | |  
QY 532 AGACTCTCTGAGAGCTGTGATTCCTTCAGAGCTTTGCTATGACATGGGTCCGC 591  
| | | | |  
Db 499 AGACTCTCTGAGAGCTGTGATTCCTTCAGAGCTTTGCTATGACATGGGTCCGC 558  
| | | | |  
QY 592 CAGGCTCTAGGCAAGGGCTGAGTGGGTGGAGTATATCATATGATGAGAGCACTTAA 651  
| | | | |  
Db 559 CAGGCTCTAGGCAAGGGCTGAGTGGGTGGAGTATATCATATGAGAGAGTTATAA 618  
| | | | |  
QY 652 TACTACGCACTCTCGTGAAGGGCCGATTCACATCTTCAGAGACATTTCCAGAAACAG 711  
| | | | |  
Db 619 TATAAGGTAGACTTCAGAAAGGGCGCACTACCATCTCCAGAGACATTTCCAGAAACAG 678  
| | | | |

Qy 712 GTGATCTPAAAAATGAACAGCCTGAGAACTGAGACAGCGCTGTCTATTACTGTGGAG 770  
Db 679 CTGTATTGGAAATGAACAGCCTGAGAACTGAGACAGCGCTGTCTATTACTGTGGAG 737

RESULT 6  
BD222938  
LOCUS BD222938 1630 bp DNA linear PAT 17-JUL-2003  
DEFINITION Heteromnibodies.  
ACCESSION BD222938  
VERSION BD222938.1 GI:33032708  
KEYWORDS JP 2002521053-A/32.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 1630)  
AUTHORS Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F.  
TITLE Heteromnibodies  
JOURNAL Patent: JP 2002521053-A 32 16-JUL-2002;  
MICROMET AG

COMMENT  
OS Homo sapiens (human)  
US Mus musculus (mouse)  
PN JP 2002521053-A/32  
PD 16-JUL-2002  
PF 28-JUL-1999 JP 2000562401  
PI 28-JUL-1998 EP 98114082.5  
PI PETER KUFER, TORSTEN DREIER, PATRICK A BAEUERLE, KATRIN BORSCHERT,  
PI FLORIAN ZETTL  
PC C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,  
PC C07K19/00,  
PC C12N5/10,C12P21/02,G01N33/53,G01N33/53/(C12N5/10,C12R1:91),  
PC (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,  
PC (C12N5/00,C12R1:91)  
CC Heteromnibodies  
FH Key  
FT CDS Location/Qualifiers  
1..1630  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 48.5%; Score 445; DB 6; Length 1630;  
Beet Local Similarity 76.3%; Pred. No. 7.6e-114;  
Matches 620; Conservative 0; Mismatches 145; Indels 48; Gaps 4;

Qy 52 GCTACCGTTGCCAGCGCCGATATTGTGTGACGCGAGTCTCCAGGACCCCTGCTTTGCT 111  
Db 78 GCTACAGGTGTACATCTCCAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCT 137

Qy 112 CCAGGGGAAAGACCACTCTCTCTGACAGGGCAGTCAAGAGTTAGTAGAGCTACTTA 171  
Db 138 GTAGAGACAGAGTACCATCTCTGCGGGGCAAGTCAAG--CATTAGACGCTATTTA 194

Qy 172 GCGTGTACAGCAGCAAACTGGCCAGGCTCCAGGCTCTCATCTATGATGTCATCCACC 231  
Db 195 AATTGTATCAGCAAAACAGGACAGGCTCTTAAGTGTCTATTATCGGGCATCTACC 254

Qy 232 AGGGCACTGGCATCCAGACAGGTTTCAGTGGCAATGGGTCCGGACAGACTTCACTCTC 291  
Db 255 CGGGAAATCGGGGCTCCAGACGATTCAGCGGCAATGATCTGGGCAAAATTACCTCTC 314

Qy 292 ACCATCAGTACAGCTGAGAGCTGAAGATTGTCAGTGTATTACTGTACAGAGTATGAGC 351  
Db 315 ACCATCAGAGCTCTGAGCTGAGATTTTGTCTACTTACTTTTGTCAACAGTCTACAGT 374

Qy 352 TCACCTCAGACACCTCAGATCACTTTGGCGGAGGAGCAAGAGTGAATCAAGAACT 411  
Db 375 TTGCC-----GATCACCCTTGGGCCAAGGAGACAGCATGTGACATTCAA----- 416

Qy 412 GTGCTGACACATCTGTCTGTGGCGGTGGCGGTTCCGAGAGTGTGATCAGGTGAGGT 471  
Db 417 -----GGAGAGAGAGATCAGGTGTGTGTGTGATCGGCGCGGC 455

Qy 472 GGCTCCAGAGTGCAGCTGGTGAAGTCTGGGGAGAGCGGTGTCACGCTGGAGGTCTCTG 531  
Db 456 GGTGAGAGGTGTGACACTGTGTGAGTCTGGGGAGAGCGGTGTCAAGCTGGAGGTCTCTG 515

Qy 532 AGACTCTCTGTGACAGCTCTGTGATTTCCCTTCAGAGACTTTGCTATGACATGGGTCCGC 591  
Db 516 AGACTCTCTGTGACAGCTCTGTGATTTCACTTCAAGTACTATGGCATGCACTGGGTCCGC 575

Qy 592 CAGGCTCAGCAAGAGGGCTGAGAGGGGTGAGGTGAGTATATCATATGATGAGCACTAA 651  
Db 576 CAGGCTCAGCAAGAGGGCTGAGAGGGGTGAGGTGAGTATATCATATGATGAGCACTAA 635

Qy 652 TACTACGAGACTCCGTTGAGAGGGCCGATTCACATCTCCAGAGACATTCAGAAACAGC 711  
Db 636 TACTATGAGACTCCGTTGAGAGGGCCGATTCACATCTCCAGAGACATTCAGAAACAGC 695

Qy 712 GTGATCTPAAAAATGAACAGCCTGAGAACTGAGACAGCGCTGTCTATTACTGTGGAGA 771  
Db 696 CTGTATCTGAAATGAACAGCCTGAGAGCTGAGACAGCGCTGTCTATTACTGTGGAGA 755

Qy 772 GATCAGACCTGTTGGGTGACT-----ATGACCACTACTAGCTTTGACGTTGGGGC 825  
Db 756 GATATGGGTGGGGGAGGTGAGGCTGAGACCTTACTACTACTAGGTATGACGTTGGGGC 815

Qy 826 AAGGAGCACAGGTCACGCTCTCTCAGAGATCC 858  
Db 816 CAGGAGCACAGGTCACGCTCTCTCAGGAAAC 848

RESULT 7  
BD222939  
LOCUS BD222939 1630 bp DNA linear PAT 17-JUL-2003  
DEFINITION Heteromnibodies.  
ACCESSION BD222939  
VERSION BD222939.1 GI:33032709  
KEYWORDS JP 2002521053-A/33.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 1630)  
AUTHORS Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F.  
TITLE Heteromnibodies  
JOURNAL Patent: JP 2002521053-A 33 16-JUL-2002;  
MICROMET AG

COMMENT  
OS Homo sapiens (human)  
US Mus musculus (mouse)  
PN JP 2002521053-A/33  
PD 16-JUL-2002  
PF 28-JUL-1999 JP 2000562401  
PI 28-JUL-1998 EP 98114082.5  
PI PETER KUFER, TORSTEN DREIER, PATRICK A BAEUERLE, KATRIN BORSCHERT,  
PI FLORIAN ZETTL  
PC C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,  
PC C07K19/00,  
PC C12N5/10,C12P21/02,G01N33/53,G01N33/53/(C12N5/10,C12R1:91),  
PC (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,  
PC (C12N5/00,C12R1:91)  
CC Heteromnibodies  
FH Key  
FT CDS Location/Qualifiers  
1..1630  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN

	Query Match	48.5%;	Score 445;	DB 6;	Length 1630;	
	Best Local Similarity	76.3%;	Pred. No.7-114;			
	Matches 620; Conservative	0;	Mismatches 145; Indels	48; Gaps	4;	
OY	52 GCATCCGTTGCCACAGCGCCTCATATTGGTGTGAAGCAAGTCCTCCAGGACCCTGTCTTGCT	111				
Dd	78 GGTAAGAAGTAGAATACTCCAGAGCTCCAGATGAAACCAGACTCCATCTCCCTCTGTGCATCT	137				
OY	112 CCAAGGAAAAGAACCACTCTTCCTGACAGGSCAGTCAAGGTGTATGACAGCTACTTA	171				
Dd	138 GTAGAGACAAGATCACCATCACTTGCAGGACAGTCAAG---ATTAGCAGCTAATTTA	194				
OY	172 GCCTGGTACACACAGAAACCTGACCAAGGCTCCAGGCTCCATCTAATGSGCATCCACC	231				
Dd	195 AATTGGATFACAGCAAACACAGAACAGCTCTTAAGCTGCTCATTTACGCGCATCTAC	254				
OY	232 AGGGCCACTGGCATGCGACAGACAGTTCACTGGCAGTGGGTCCGGACACACTTCACTCTC	291				
Dd	255 CGGGAAATCCGGGGTCCCTGACCGATTACAGCGCAGTGAATCGGACAATTAACCTCTC	314				
OY	292 ACCATCAAGTAGACTGAGCGCTGAABATTTTTGCAAGTATTACTGACAGATATGATAGC	351				
Dd	315 AACATCAGAGCCTGAGCTGAAAGATTTTGCTACTTCTTTTGCACAAGCTGACAGT	374				
OY	352 TCACCTCAGACACTCAGATCACTTTCGGCGAGGAGCAAGAGTGGATCAAAAGAACT	411				
Dd	375 TTGCC-----GATCACCTTCGGCCAAAGGACACGACTGGACATTCAC-----	416				
OY	412 GTGGCTGACCAATCTGTCTCTGCGCGGTGCGGCTTCGAGGTGTGTATCAGTGGAGT	471				
Dd	417 -----GGAGAGAGAGATCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	455				
OY	472 GGCTCCCAAGTCACTGGTGTGAGTCTGAGGGAGGCGTGTCCAGCTGGAGAGTCCCTG	531				
Dd	456 GGCTCAGAGTGTCACTGCTGTGAGTCTGTGGGAGGCGTGTGTCCAGCTGGAGAGTCCCTG	515				
OY	532 AGACTCTCCTGTGCAGCCTCTTGATTTCCCCTTCAGAACTTTGCTATGCACTGGGTCCG	591				
Dd	516 AGACTCTCCTGTGCAGCCTCTTGATTTCACTTCAGTACTATGAGCATGCACTGGGTCCG	575				
OY	592 CAGGCTCAGGAAAGGGGCTGAGTGGGTGGAGCATATATCATATGATGAGAAACACTTAA	651				
Dd	576 CAGGCTCAGGAAAGGGGCTGAGTGGGTGGAGCATATATCATATGATGAGAAAGTAA	635				
OY	652 TACTACGCAACTCCGTGAAGGGCCGATTCAACATCTCCAGAGCACTTCCAAAGAACG	711				
Dd	636 TACTATGCAACTCCGTGAAGGGCCGATTCAACATCTCCAGAGCAATTTCAAAGAACG	695				
OY	712 GTGTATCTAAAAATGAACAGCTTGAACTGAGACACAGGCTGTCTATTACTGTGCGAGA	771				
Dd	696 CTGTATCTGCAAAATGAACAGCTTGAGACTGAGACAGGCTGTGTATTACTGTGCGAAA	755				
OY	772 GATCAGACCTGTTGGTGTGACT-----ATGACCACTACTAAGGTTTGGAGCTCCGAGGC	825				
Dd	756 GATATGGGGTGGGAGAGTGCTGAGAGACCTCACTACTACTACGGTATGAGAGTCTGGGC	815				
OY	826 AAAAGGACCAAGCTACCGCTCTCTCCAGAGATCC	858				
Dd	816 CAAGGAGCAACGCTACCGCTCTCTCCGGAACC	848				
RESULT 8 AXO23365						
LOCUS	AXO23365	1630 bp	DNA	linear	PAT 15-SEP-2000	
DEFINITION	Sequence 36 from Patent WO0006605.					
ACCESSION	AXO23365					
VERSION	AXO23365.1	GI:10183777				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
REFERENCE	1					

AUTHORS		TITLE		JOURNAL		FEATURES	
Kufner, P., Zettl, F., Dreier, T., Baeuerle, P. A. and Bortschert, K.		Heteromindibodies		Patent: WO 0006605-A 36 10-FEB-2000;		DREIER TORSTEN (DE)	
KUFNER PETER (DE)		ZETTL FLOSIAN (DE)		BAEURLER PATRICK A (DE)		BORSCHERT KATRIN (DE)	
MICROWET GES FUER BIOMEDIZINIS (DE)		location/Qualifiers		1..1630			
source		/organism="Homo sapiens"		/mol_type="unassigned DNA"		/db_xref="taxon:9606"	
CDS		39..1610		/note="unnamed protein product"		/codon_start=1	
		/protein_id="CAC08835.1"		/db_xref="GI:10183778"		/translation="MGWSCTILFLVATATGSHLQMTQSPSSLSASVGDRTVITGRA	
						SOSLSISYLMNYOQKGPRLILYMSTRSGVDPDRSGESSTNTVLTLSIQEPF	
						ATYCOOSDLPFPGQGTRLIDQGGSGSGGSGGGSVOLLESGGVQVGRSLR	
						LSCGASPTSSVGMHVRQAPGKGMKMWAVISYDSNKYVADSVMGRFLTISDNGN	
						TLTIQNSLSIAEDPIAAVYCYCAKDMGSGMGRPYVYIGMDVYQSGTLYVSGSGPT	
						HTASTKQPSVFPPLAPSSKTSSTGTAALGCLVAKYFPPVTVSNMGSALTSVHTFPV	
						LQSSGLVSLSSVTVTPSSLSGTQIYICNVNHRKSNKTKVDKVRPKSCDKTSGGGSSAP	
						ARSSPSSTQPMWENVAIOEARLDLINTSRDPAAMNENIVEVISMFLDQETVQIOTLE	
						LYKQGLGSLTKLKGPLTMMASHYKQHCPTPETSCATQIITFESEKEMIKDPLIVIP	
						FDCEWPEQEHNNHHH"	
ORIGIN							
Query Match		48.5%		Score 445;		DB 6;	
Best Local Similarity		76.3%		Pred. No. 7.6e-114;		Indels 48;	
Matches 620;		Conservative 0;		Mismatch 145;		Gaps 4;	
QY	52	GCTACCGTTGGCGAGCGCGCATATGTGTTTACGACGAGTCTCCAGAGCACTGTCTTGTCT	111				
DB	78	GCTACAGGTGACACTCCGAGCTCCAGATACCAAGCTCTCATCTCCCTGTCTGCATCT	137				
QY	112	CCAGGGGAAAGCCACCCCTCTCTCTGCAAGGCGCAGTCAAGTGTATGATGACGACTTA	171				
DB	138	GTAGAGACAGAGTCACCATCATCTTGGCGGGAAGTCAAG---CATTAGCACCTATTTA	194				
QY	172	GCCTGTATACGACGAGAAACCTGGCGCAGGCTCCAGAGCTCCTCATATGATGGATGCAC	231				
DB	195	AATTGTATACGACGAGAAACAGAGACAGCTCTTAAGTGTCTCATTTACTGGGACTTACC	254				
QY	232	AGGGCCACTGCGATGCGACAAGGTTTCAGTGGCAGTGGAGTCCGGGACAGACTTCACTTC	291				
DB	255	CGGGAATCCGGGGTCTCTGACCAATTCAGGGGCAAGTGAATCTGGGCAAAATTACACTTC	314				
QY	292	ACCATGATGACGTGCGAGCTGGAAGATTGGTCAGTGTATATACGTGACAGTATGTGATGC	351				
DB	315	ACCATGACAGCTGCGAGCTGGAAGATTGTGCTACTTATCTTGTCAACGTGTGACAGT	374				
QY	352	TCACCTGACACACTCGATCACTTTCGCGGAGGGGACCAAGGTGAGAGATCAAAACAAC	411				
DB	375	TTGGC-----GATCACTTCCTGGCCAAAGGGACACGACTGACATTCAA-----	416				
QY	412	GTGGCTGACCATTTGCTCTCTGGCGGTGGCGGTTCCGAGAGTGTGTGATCAGGTGAGGT	471				
DB	417	-----GAGAGGAGGAGATCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	455				
QY	472	GGCTCCAGGTCAGCTGTGTGAGTCTGGGGGAGGCGTGGTCCAGCTCGGAGAGTCCCTG	531				
DB	456	GGCTCAAGGTGACGTGCTCGAGTCTGGGGGAGGCGTGTCCAGCTCGGAGAGTCCCTG	515				
QY	532	AGACTCTCTGTGACGCTCTGGAATTCCTCTTCAAGAGCTTTGTCTATGCACTTGGGTCCG	591				
DB	516	AGACTCTCTGTGACGCTCTGGAATTCCTTCAAGTGTATGTGACGACTGGGTCCCG	575				
QY	592	CAGGCTCTAGGCAAGGGGCTGAGTGGGTGGGAGTATATCATATGATGGAAGCACTAA	651				
DB	576	CAGGCTCAGGCAAGGGGCTGAGTGGGTGGGAGTATATCATATGATGGAAGCACTAA	635				
QY	652	TACTACGACACTTCGTGAAGGGCGAATTCACCATCTCCAGAGACACTTCCAAAGACAG	711				

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	REFERENCE	AUTHORS
AP416910	867 bp mRNA linear SYN 22-OCT-2003	AF416910									
AP416910	Synthetic construct JB-43 recombinant single chain Fv antibody derivative mRNA, partial cds.	AF416910									
AP416910.1	GI:16033614										
	Synthetic construct										
	synthetic construct										
	other sequences; artificial sequences.										
	(bases 1 to 867)										
	Bangale, Y., Cavill, D., Gordon, T., Planque, S., Taguchi, H.,										
	Bhatia, G., Nishiyama, Y., Arnett, F. and Paul, S.										
	Vasoactive intestinal peptide binding autoantibodies in autoimmune										
	humans and mice										
	Peptides 23 (12), 2251-2257 (2002)										
	2 (bases 1 to 867)										
	Bangale, Y., Li, L., Cavill, D., Gordon, T., Karle, S., Planque, S.,										
	Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and										
	Paul, S.										
	Broad distribution and disease association of vasoactive intestinal										
	peptide binding and cleaving autoantibodies										
	Unpublished										
	3 (bases 1 to 867)										
	Bangale, Y., Li, L., Cavill, D., Gordon, T., Karle, S., Planque, S.,										
	Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and										
	Paul, S.										
	Broad distribution and disease association of vasoactive intestinal										
	peptide binding and cleaving autoantibodies										
	Unpublished										
	3 (bases 1 to 867)										
	Bangale, Y., Li, L., Cavill, D., Gordon, T., Karle, S., Planque, S.,										
	Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and										
	Paul, S.										
	Broad distribution and disease association of vasoactive intestinal										
	peptide binding and cleaving autoantibodies										
	Unpublished										
	3 (bases 1 to 867)										
	Bangale, Y., Li, L., Cavill, D., Gordon, T., Karle, S., Planque, S.,										
	Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and										
	Paul, S.										
	Broad distribution and disease association of vasoactive intestinal										
	peptide binding and cleaving autoantibodies										
	Unpublished										
	3 (bases 1 to 867)										
	Bangale, Y., Li, L., Cavill, D., Gordon, T., Karle, S., Planque, S.,										
	Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and										
	Paul, S.										
	Broad distribution and disease association of vasoactive intestinal										
	peptide binding and cleaving autoantibodies										
	Unpublished										
	3 (bases 1 to 867)										
	Bangale, Y., Li, L., Cavill, D., Gordon, T., Karle, S., Planque, S.,			</							











```

Db      373 ATCAGCTTGGCGGAGGACCAAGGTGAGATCAACAGACTGTGCTGCACCATCTGTC 432
Qy      430 T 430
Db      433 T 433

RESULT 15
LOCUS   MMAPJ5051
DEFINITION Mus musculus VSV-IND neutralising scFv antibody fragment generated from the germline precursor of antibody V124.
ACCESSION AJ005051
VERSION AJ005051.1 GI:3123634
KEYWORDS scFv fragment; V124 antibody.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Kallinke, U. and Lamarre, A.
  In vitro affinity maturation of VSV-specific single-chain Fv
  antibody fragments
  JOURNAL Unpublished
  REFERENCE 2 (bases 1 to 790)
  AUTHORS Kallinke, U.
  TITLE Direct Submission
  JOURNAL Submitted (30-MAR-1998) Kallinke U., Institute of Experimental
  Immunology, Department of Pathology, Schmelzbergstr. 12, 8091
  Zuerich, SWITZERLAND
  COMMENT Related sequence: X97498.
  FEATURES
    source location/Qualifiers
      1..790
        /organism="Mus musculus"
        /mol_type="mRNA"
        /strain="BALB/c"
        /db_xref="taxon:10090"
        /cell_line="germline precursor of V124"
        /cell_type="hybridoma"
      1..790
        /note="VSV-IND neutralising scFv fragment"
      misc_feature 20..31
        /note="DYKD FLAG-tag"
      V_region 29..367
        /note="light chain"
      misc_feature 368..427
        /note="(GlyGlyGlyGlySer)x4 flexible linker"
      V_region 428..778
        /note="heavy chain"

ORIGIN
Query Match 39.0%; Score 358.4; DB 10; Length 790;
Best Local Similarity 71.6%; Pred. No. 1.8e-89;
Matches 530; Conservative 0; Mismatches 171; Indels 39; Gaps 3;

Qy      70 GATATGTGTGACGACAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGACCAACC 129
      29 GACATTGTGATGTCAACAGTCTCCATCTCTCCAGTGTCTGAGAGAGAGTTACT 88
Qy      130 CTCTCTGAGGGCCAGTCAAGTGTAGTACAG-----CTACTTAGCC 174
      89 ATGAGCTGCAGAGTCAAGTCAAGAGCTTTATATAGTCAATCAAAAGAACTAATGGCC 148
Qy      175 TGGTACGACGAAACCTGGGCGAGGCTCCAGGCTCCATCTATGAGTCAATCCACGAG 234
      149 TGGTACGACGAAACCTGGGCGAGGCTCCATCTAATCTGATTTACTGGGCAATCCACTAG 208
Qy      235 GCCACTGGCATCCAGACAGTTCAGTGGCAGTGGGCTCCGGGACAGACTTCACTCTACC 294
      209 GAATCTGGGGGCTCCGTGATGCTTCAAGGCAATGAGATCTGGGACAGATTTCACCTCAC 268
Qy      295 ATCAGTAGCTGAGAGCTGAAGATTTTGCAGTGTATTACTGTACAGAGTATGTAAGTCA 354

```

```

Db      269 ATCAGAGTGTAAAGCTGAAAGACCTGGAGTTTATTACTGTACAGCAATATTATAGCT-- 326
Qy      355 CCTCAGACACCTCAGATCACTTTCGCGGAGGACCAAGGTGAGATCAAAAGAACTGTG 414
      327 -----ATTACAGCTTCGAGGGGGGACCAAGCTGGAAATAAAGTGTGTGT 373
Qy      415 GCTGACCAATCTGTCTTGGCGGTGGCGGTTCCGAGAGGTGTGATCAGGTGAGGTGC 474
      374 G-----GTGGTTCTGGCCGCGCGGCTCCGAGGTGTGATCCGAGGTGAGGT 424
Qy      475 TCCAGGTGAGCTGTGAGTCTGGGGAGGCGGTGTCACAGCTGGAGAGTCCCTGANA 534
      425 TCCAGTGTGAGCTGTGAGTCTGGGGAGGCTTAGTGTGACCTGGAGAGGTCCGANA 484
Qy      535 CTCTCTGTGACGCTCTGATTTCCCTTCAGAACTTTGCTATGCACTGGGTCCGCGAG 594
      485 CTCTCTGTGACGCTCTGAGATTCACTTTCACTTTGGAAATGCACTGGGTTCGTGAG 544
Qy      595 GCTTAAAGCAAGGGGCTGAGTGGGTGGCAATTATATATATATATATATATATATATAT 654
      545 GCTTCAAGAAAGGGGCTGAGTGGGTGGCAATTATATATATATATATATATATATATAT 604
Qy      655 TACGAGACTCCGTGAAGGCGGATTCACCAATCTCCAGAGACACTTCCAAAGAACGCTG 714
      605 TATGACAGACAGTGAAGGCGGATTCACCAATCTCCAGAGACACTTCCAAAGAACGCTG 664
Qy      715 TATCTAAATGAACAGCTGAGAACTGAGACAGGCTGTCTATTACTGTGCGAGAGAT 774
      665 TTCTCTGAAATGACAGCTTAAAGTCTAGAGACAGGCAATGATATTACTGTGCAAGATG 724
Qy      775 CAGAGCTGTGGGTGACTA 794
      725 GGGGGTACTACTTGACTA 744

```

Search completed: February 18, 2005, 07:22:11  
Job time : 4381 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 04:03:21 ; Search time 616 Seconds

(without alignments)  
8821.952 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 918  
Sequence: 1 GAATTCATGTAAGAAAAACCGC.....ATCACCATTAGTGAAGCTT 918

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16dec04:\*  
1: geneeqn19808:\*  
2: geneeqn19908:\*  
3: geneeqn20008:\*  
4: geneeqn20018:\*  
5: geneeqn20028:\*  
6: geneeqn20038:\*  
7: geneeqn20048:\*  
8: geneeqn20058:\*  
9: geneeqn20068:\*  
10: geneeqn20078:\*  
11: geneeqn20088:\*  
12: geneeqn20098:\*  
13: geneeqn20108:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	2	AAV10118 Human H11
2	918	100.0	918	4	AAO04537 Human mon
3	918	100.0	918	9	ACA62168 C-antigen
4	918	100.0	918	12	AD052295 Human ant
5	916.4	99.8	918	4	AAO04538 Human H11
6	916.4	99.8	918	12	AD052297 Human ant
7	799.6	87.1	867	2	AAV10119 Human H11
8	799.6	87.1	867	4	AAO04539 Human mon
9	799.6	87.1	867	9	ACA62170 C-antigen
10	799.6	87.1	867	12	AD052298 Human ant
11	798	86.9	867	4	AAO04540 Human H11
12	798	86.9	867	12	AD052300 Human ant
13	457	49.8	1103	12	ADP83553 Anti-teta
14	445	48.5	1630	3	AAZ50588 HD706CFV-
15	445	48.5	1630	3	AAZ50587 HD706CFV-
16	431.2	47.0	756	12	AD058063 S2 cell d
17	395.2	43.1	840	10	ACF58047 HIV-1 neu
18	361	39.3	450	4	AAO04530 Human H11
19	361	39.3	450	12	AD052288 Human ant
20	359.4	39.2	450	2	AAV10111 Human mon

## ALIGNMENTS

21	359.4	39.2	450	4	AAO04529	AAO04529 Human mon
22	359.4	39.2	450	9	ACA62160	ACA62160 Human C-a
23	359.4	39.2	450	12	AD052286	AD052286 Human ant
24	348.4	38.0	762	10	ADH44203	ADH44203 gfv antib
25	346.4	37.7	828	13	ADT02273	ADT02273 Human-lyp
26	345.8	37.7	1574	3	AAZ57599	AAZ57599 Erythrocy
27	345.2	37.6	783	2	AAO08490	AAO08490 Anti-CS M
28	343.6	37.4	786	10	ADH44205	ADH44205 gfv antib
29	343.6	37.4	1648	2	AAV96346	AAV96346 Chimeric
30	342.8	37.3	771	10	ADH44204	ADH44204 gfv antib
31	337.8	36.8	762	12	AD040403	AD040403 Single ch
32	336.8	36.7	741	12	AD040399	AD040399 Single ch
33	336.8	36.7	756	12	AD040396	AD040396 Single ch
34	336.8	36.7	759	12	AD040397	AD040397 Single ch
35	336.2	36.6	741	13	ADT02275	ADT02275 Human-lyp
36	335.2	36.5	756	12	AD040400	AD040400 Single ch
37	334.6	36.4	1953	9	ACR05482	ACR05482 Anti-CD7
38	334.6	36.4	1956	9	ACR05481	ACR05481 Anti-CD7
39	329	35.8	786	10	ADH44207	ADH44207 gfv antib
40	328	35.7	5227	2	AAV79537	AAV79537 Plasmid p
41	326	35.5	888	5	ACA62158	ACA62158 Single ch
42	325.4	35.4	543	9	ACA62158	ACA62158 Human C-a
43	325.4	35.4	543	12	AD052285	AD052285 Human ant
44	325.4	35.4	543	12	AD052283	AD052283 Human ant
45	324.4	35.3	543	2	AAV10110	AAV10110 Human mon

RESULT 1  
AAV10118  
ID AAV10118 standard; DNA, 918 BP.

AAV10118;  
29-MAY-1998 (first entry)

Human H11-scFv construct monomer forming DNA sequence.  
H11; monoclonal antibody; Mab; C-antigen; variable region heavy chain;  
V region; H chain; neoplasia; detection; lymphoma; tumor cell; probe;  
primer; vaccine; gene therapy; glioblastoma; neuroblastoma;  
malignant melanoma; adenocarcinoma; small cell lung carcinoma;  
single chain variable region; scFv; ss.  
Synthetic.  
Homo sapiens.

Key Location/Qualifiers  
CDS 1..918  
FT /\*tag= a  
FT /product= "H11-scFv construct"  
FT /note= "partial sequence of monomer forming construct is  
interrupted by an intron."  
FT 907..912  
FT /\*tag= b

intron  
WO9744461-A2.

27-NOV-1997.

22-MAY-1997; 97WO-US008962.

22-MAY-1996; 96US-00657449.

(NOVO-) NOVOPHARM BIOTECH INC.

Dan MD, Mail PK, Kaplan HA;

WPI, 1998-018515/02.

P-PsDB; AAM40070.

PT Antigen binding fragment from monoclonal antibody, H11 - allows tumour  
 PT specific detection and treatment of neoplasia.

XX Example 7; Page 90-91; 126bp; English.

CC This sequence encodes a human H11 monoclonal antibody single chain V  
 CC region fragment (H11-scFv) construct which is capable of forming  
 CC monomers. This construct is used to determine the ability of H11-scFv  
 CC antibody fragments to bind specifically to the C-antigen on cancer cells.  
 CC Such antigen binding fragments may be used for treating a patient with  
 CC neoplasia. It is especially useful in the detection of lymphomas and  
 CC leukemias where the tumour cells bearing the C antigen are circulating  
 CC in the patients bloodstream. The polynucleotide sequence may be used as a  
 CC primer or a probe and the encoded protein may be used in a vaccine or for  
 CC gene therapy. The human monoclonal antibody (Mab), designated H11,  
 CC specifically recognises cancerous cells. H11 is specific for  
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,  
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and  
 CC prostate adenocarcinoma

XX Sequence 918 BP; 213 A; 240 C; 264 G; 201 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 2; Length 918;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-227;  
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCCTATGCGATGCAAGTGCATGCTGGTTCGCTACCGTT 60  
 DB 1 GAATTCATGAAAAAACCCTATGCGATGCGATGCAAGTGCATGCTGGTTCGCTACCGTT 60  
 QY 61 GCGCAGGCGCATATGTTGTTGACGACGTCACAGGACCCCTGCTTGTCTCCAGGGGAA 120  
 DB 61 GCGCAGGCGCATATGTTGTTGACGACGTCACAGGACCCCTGCTTGTCTCCAGGGGAA 120  
 QY 121 AGAGCAACCTCTCTGCAAGGCGCAGTCAGAGTGTAGTAGCACTAATTAAGCTGTAC 180  
 DB 121 AGAGCAACCTCTCTGCAAGGCGCAGTCAGAGTGTAGTAGCACTAATTAAGCTGTAC 180  
 QY 181 CAGCAGAAAACTTGGCCAGGCTCCAGGCTCTCATCTATGTCATTCACACAGGCGCACT 240  
 DB 181 CAGCAGAAAACTTGGCCAGGCTCCAGGCTCTCATCTATGTCATTCACACAGGCGCACT 240  
 QY 241 GGCATCCAGACAGAGTTCAGTGGGTCGCGGACAGACTTCACTCTCACATCAAT 300  
 DB 241 GGCATCCAGACAGAGTTCAGTGGGTCGCGGACAGACTTCACTCTCACATCAAT 300  
 QY 301 AGACTGAGGCTGAAAGATTTTTCAGTGTATTAATCTGTACAGAGTATGTAGCTCACTCAG 360  
 DB 301 AGACTGAGGCTGAAAGATTTTTCAGTGTATTAATCTGTACAGAGTATGTAGCTCACTCAG 360  
 QY 361 ACAACCTCAATCACTTTTCCGCGGAGGACCAAGTGGAGATCAAGAACTGTGGTGTCA 420  
 DB 361 ACAACCTCAATCACTTTTCCGCGGAGGACCAAGTGGAGATCAAGAACTGTGGTGTCA 420  
 QY 421 CCATCTGTCTTGGCGGTGGCGGTTCCGAGGTGTGATCAGAGTGAAGTGGCTCCAG 480  
 DB 421 CCATCTGTCTTGGCGGTGGCGGTTCCGAGGTGTGATCAGAGTGAAGTGGCTCCAG 480  
 QY 481 GTGCACTGTGTGAGTCTGCGGAGGCGGTGTCTCAAGCTTGGAGAGTCCCTGAGACTTCC 540  
 DB 481 GTGCACTGTGTGAGTCTGCGGAGGCGGTGTCTCAAGCTTGGAGAGTCCCTGAGACTTCC 540  
 QY 541 TGTGCACTGTGTGAGTCTTCCCTTCAAGAGCTTGTGATCACTGGGTCCGCGAGGCTCTCA 600  
 DB 541 TGTGCACTGTGTGAGTCTTCCCTTCAAGAGCTTGTGATCACTGGGTCCGCGAGGCTCTCA 600  
 QY 601 GGCAGAGGCGCTGAGTGGTGTGCAATTATCATATGATGAGAACTAATACTACGCA 660  
 DB 601 GGCAGAGGCGCTGAGTGGTGTGCAATTATCATATGATGAGAACTAATACTACGCA 660  
 QY 661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTCGAGAAACGGGTATCTTA 720  
 DB 661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTCGAGAAACGGGTATCTTA 720

QY 721 AAAATGAACAGCCTGAGAACTGAGGACACGGCTGTCTATTACTGTGCGAGATCAGAGC 780  
 DB 721 AAAATGAACAGCCTGAGAACTGAGGACACGGCTGTCTATTACTGTGCGAGATCAGAGC 780  
 QY 781 CTTGTTGGGAGTATGACCACTACATAGGTTTGAACGTCTGGGGCAAGGGGCAACGGTTC 840  
 DB 781 CTTGTTGGGAGTATGACCACTACATAGGTTTGAACGTCTGGGGCAAGGGGCAACGGTTC 840  
 QY 841 ACCGTCCTCTCAGATTCGCAACAAAACCTGATCAGCGAAGAGATCTGAACCATCAGCAT 900  
 DB 841 ACCGTCCTCTCAGATTCGCAACAAAACCTGATCAGCGAAGAGATCTGAACCATCAGCAT 900  
 QY 901 CACCATTAAGTGAAGCTT 918  
 DB 901 CACCATTAAGTGAAGCTT 918

# RESULT 2

AAD04537  
 ID AAD04537 standard; DNA; 918 BP.

XX AAD04537;

XX 04-JUL-2001 (first entry)

XX Human monoclonal antibody H11-single chain variable region (scFv) DNA #1.

XX Human; monoclonal antibody; Mab; H11; single chain variable region; scFv;

XX neoplastic disease; melanoma; immunoglobulin IGM; gene therapy; lymphoma;

XX carcinoma; breast; lung; gastric; prostate; prostate; ovary; colon; lung; vaccine;

XX C-antigen; chronic leukemia; glioma; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..918

FT /product= "Human H11-single chain variable region (scFv)"

FT /transl\_except= (pos:904..915, aa:His-Lys)

FT /note= "Insertion of two inframe stop codon alters the reading frame; CDS does not include start and stop codons"

FT misc\_feature /partial 430..474

FT /tag= b

FT /note= "Encodes (SGGG) 3 linker sequence"

PN US6207153-B1.

PD 27-MAR-2001.

PF 22-MAY-1997; 97US-00862124.

PR 22-MAY-1996; 96US-00657449.

PA (VIVE-) VIVENTIA BIOTECH INC.

PI Dan MD, Maici PK, Kaplan HA;

PI MPI: 2001-289584/30.

DR P-PSDB; AAE00947.

PT Composition comprising antigen binding fragments of an antibody that

PT recognizes an antigen on neoplastic cells but not on normal cells for use

PT in diagnosis, imaging and treatment of carcinomas.

PS Example 7; Col 61-64; 56bp; English.

XX The present DNA sequence encodes human monoclonal antibody (Mab), H11-  
 CC single chain variable region (scFv). The H11 light chain variable region  
 CC is linked to the heavy chain variable region through a (SGGG) 3 linker to

CC form monomers. The invention relates to human monoclonal antibody (Mab)  
 CC H11, H11-(scFv) single chain variable (V) region fragment and their  
 CC corresponding DNA molecules. H11 antibody is an immunoglobulin of 19M  
 CC subunits which is specific to C-antigen found specifically on neoplastic  
 CC cells and not on normal cells. H11 is an antibody obtained from the  
 CC fusion of peripheral blood lymphocytes of a 64 year old male with a low  
 CC grade glioma and fused to a human myeloma cell line to produce a  
 CC hybridoma designated NBGM1/H11. A pharmaceutical composition comprising  
 CC H11 and its derivatives are useful in the diagnosis, imaging and  
 CC treatment of neoplastic disease, particularly, melanoma, breast  
 CC carcinoma, lung carcinoma, ovarian carcinoma, colon carcinoma, gastric  
 CC carcinoma, prostate carcinoma, lymphoma carcinoma, neuroblastoma, glioma,  
 CC soft tissue sarcoma, small cell lung carcinoma, prostatic adenocarcinoma,  
 CC B and T cell lymphomas and chronic leukaemias. H11 DNA is also used in  
 CC vaccines and gene therapy  
 XX  
 XX Sequence 918 BP; 213 A; 240 C; 264 G; 201 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 918; DB 4; Length 918;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-227;  
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCCTATCCGATCGCATGTCATGCTGCTGCTACCGTT 60  
 DB 1 GAATTCATGAAAAAACCCTATCCGATCGCATGTCATGCTGCTGCTACCGTT 60  
 QY 61 GCGCAGCCGATATTTGTGTTGACGAGTCTCAAGCACCCTGCTTTGTCTCCAGGGAA 120  
 DB 61 GCGCAGCCGATATTTGTGTTGACGAGTCTCAAGCACCCTGCTTTGTCTCCAGGGAA 120  
 QY 121 AGAGCACCCTCTCTGCGAGGGCCGATCGAGTGTAGTAGAGCACTTACCTGTGTC 180  
 DB 121 AGAGCACCCTCTCTGCGAGGGCCGATCGAGTGTAGTAGAGCACTTACCTGTGTC 180  
 QY 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGTCATCCACAGGCGCACT 240  
 DB 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGTCATCCACAGGCGCACT 240  
 QY 241 GGCATGCCAGACAGGTTCAGTGCGCAGTGGGTCCGGACAGACTTCACTCCACATCACT 300  
 DB 241 GGCATGCCAGACAGGTTCAGTGCGCAGTGGGTCCGGACAGACTTCACTCCACATCACT 300  
 QY 301 AGACTGGAGCCGTGAAGATTTTGGCAGTGTATTACTGTCCAGCACTATGTGATGCTCAGCTGAG 360  
 DB 301 AGACTGGAGCCGTGAAGATTTTGGCAGTGTATTACTGTCCAGCACTATGTGATGCTCAGCTGAG 360  
 QY 361 ACACCTCAGATCACTTTCGCGCGAGGAGCAAGAGTGAAGATCAAAAGAACTGTGGCTGCA 420  
 DB 361 ACACCTCAGATCACTTTCGCGCGAGGAGCAAGAGTGAAGATCAAAAGAACTGTGGCTGCA 420  
 QY 421 CCATCTGTCTCTGCGCGTGGCGGTTCCGGAGGTGTGATCAAGTGAAGTGGCTCCGAG 480  
 DB 421 CCATCTGTCTCTGCGCGTGGCGGTTCCGGAGGTGTGATCAAGTGAAGTGGCTCCGAG 480  
 QY 481 GTGCGAGTGTGAGATCTGCGGGGAGCGGTGTCCAGCCTGGGAGGTCTCCAGACTCTCC 540  
 DB 481 GTGCGAGTGTGAGATCTGCGGGGAGCGGTGTCCAGCCTGGGAGGTCTCCAGACTCTCC 540  
 QY 541 TGTGACGCTCTGATGATCCCTTCAAGAACTTGTCTATGACATCGGCTCCGAGGCTCTA 600  
 DB 541 TGTGACGCTCTGATGATCCCTTCAAGAACTTGTCTATGACATCGGCTCCGAGGCTCTA 600  
 QY 601 GGCAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAAAGCACTAAATATCAAGCA 660  
 DB 601 GGCAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAAAGCACTAAATATCAAGCA 660  
 QY 661 GACTCCGTAAGGGCGGATTCACCATCTCCAGAGACATTCACAAAGACCGTGTATCTA 720  
 DB 661 GACTCCGTAAGGGCGGATTCACCATCTCCAGAGACATTCACAAAGACCGTGTATCTA 720  
 QY 721 AAAATGAACAGCCTGAGAACTGAGACACGCGTGTCTATTAATGTGCGAGATCAGAGC 780  
 DB 721 AAAATGAACAGCCTGAGAACTGAGACACGCGTGTCTATTAATGTGCGAGATCAGAGC 780

QY 781 CTGTTGGTGACTATGACCACTACTACGCTTTGACGCTTGGGCGCAAGGAGCACAGCTC 840  
 DB 781 CTGTTGGTGACTATGACCACTACTACGCTTTGACGCTTGGGCGCAAGGAGCACAGCTC 840  
 QY 841 ACCGTCCTCGTGGATCCGACAAAACGATCAGCGAAGAGATCTGAACATCAGCAT 900  
 DB 841 ACCGTCCTCGTGGATCCGACAAAACGATCAGCGAAGAGATCTGAACATCAGCAT 900  
 QY 901 CACCATTTAGTGAAGCTT 918  
 DB 901 CACCATTTAGTGAAGCTT 918  
 CC  
 CC AC62168  
 CC ID AC62168 strand; DNA; 918 BP.  
 CC  
 CC AC62168;  
 CC  
 CC 07-AUG-2003 (first entry)  
 CC  
 CC C-antigen antibody H11 single chain variable region fragment #1 DNA.  
 CC  
 CC Human; ds; gene; H11; single chain variable region; gene therapy; scFv;  
 CC neoplasia; tumour; recurrence risk; C-antigen; melanoma; neuroblastoma;  
 CC glioma; soft tissue sarcoma; small cell lung carcinoma; brain cancer;  
 CC C-antigen specific antibody; alphac; vaccine; cancer.  
 CC  
 CC Homo sapiens.  
 CC  
 CC Synthetic.  
 CC  
 CC Key Location/Qualifiers  
 CC FT 1..918  
 CC CDS /\*tag= a  
 CC FT /partial  
 CC FT /product= "H11 single chain variable region fragment #1"  
 CC FT /transl\_except= (pos:904..915,aa:His-Lys)  
 CC FT /note= "No start or stop codon given"  
 CC  
 CC US2003021779-A1.  
 CC  
 CC 30-JAN-2003.  
 CC  
 CC 13-FEB-2001; 2001US-00782397.  
 CC  
 CC 22-MAY-1996; 96US-00657449.  
 CC 22-MAY-1997; 97US-00862124.  
 CC  
 CC (DANM/) DAN M D.  
 CC (MAIT/) MAITI P K.  
 CC (KAPL/) KAPLAN H A.  
 CC  
 CC Dan MD, Maici PK, Kaplan HA;  
 CC  
 CC WPI; 2003-456278/43.  
 CC P-PSDB; ABU10486.  
 CC  
 CC Novel antigen binding fragment of monoclonal antibody specific for  
 CC antigen detected on neoplastic cells, useful for diagnosing or treating  
 CC cancer, for manufacturing novel reagents and as diagnostic and imaging  
 CC reagent.  
 CC  
 CC Example 7; Page 32-33; 62pp; English.  
 CC  
 CC The invention relates to a polypeptide which is an antigen binding  
 CC fragment of a monoclonal antibody specific for an antigen detected on  
 CC neoplastic cells. The antigen binding fragment (ABF) is useful for  
 CC treating a patient with a neoplasia. The individual has a clinically  
 CC detectable tumour. The method is useful for palliating the neoplasia. The  
 CC method reduces the risk of recurrence of a clinically detectable tumour.  
 CC The antigen binding fragment is labelled with a therapeutic moiety such  
 CC as radioisotopes or immunomodulators. ABF is useful for detecting C-

CC antigen in a sample. The polypeptide is useful for diagnosing, localising  
CC and/or treating neoplasias, including melanoma, neuroblastoma, glioma,  
CC soft tissue sarcoma and small cell lung carcinoma. The polypeptide is  
CC useful for manufacturing novel reagents and for treating and imaging  
CC brain cancer. ABF is useful as a diagnostic and imaging reagent. The  
CC composition is useful for eliciting an immune response against neoplasia.  
CC The polynucleotide is useful in expression systems for the production of  
CC C-antigen specific antibody, termed H11 or alphac, as hybridisation  
CC probes to assay for the presence of alphac polynucleotide or related  
CC sequences in a sample, as primers to effect amplification of desired  
CC polynucleotides and in pharmaceutical compositions including vaccines and  
CC for gene therapy. The polynucleotide is also useful for genetically  
CC altering cells in vivo, thus treating various types of cancer. The  
CC polypeptide, polynucleotide and the composition are useful for detecting  
CC or treating cancer, including the therapy of cancer and prophylactic care,  
CC particularly for decreasing the risk of recurrence. The present sequence  
CC represents the human C-antigen specific antibody H11 single chain  
CC variable region fragment, scFv, #1 DNA

XX Sequence 918 BP; 213 A; 240 C; 264 G; 201 T; 0 U; 0 Other;

SO Query Match 100.0%; Score 918; DB 9; Length 918;

Best Local Similarity 100.0%; Pred. No. 1.8e-227;

Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCCGCTATCGCGATCGAGTTCGCTGGTTCGCTACCGTT 60  
DB 1 GAATTCATGAAAAAACCCGCTATCGCGATCGAGTTCGCTGGTTCGCTACCGTT 60  
QY 61 GCGCAGACCGCATATGTGTGACGCGAGTCTCCAGGACCCCTGTTGTCTCCAGGGGAA 120  
DB 61 GCGCAGACCGCATATGTGTGACGCGAGTCTCCAGGACCCCTGTTGTCTCCAGGGGAA 120  
QY 121 AAGAGCCACCTCTCTGTCAGGGGCGAGTCAAGGTGTTAGTACGCTTACCTTGCTGAC 180  
DB 121 AAGAGCCACCTCTCTGTCAGGGGCGAGTCAAGGTGTTAGTACGCTTACCTTGCTGAC 180  
QY 181 CAGGCAAAACCTGGCCAGGCTCCAGGCTCCATCATATGTCGATCCACAGGGCACT 240  
DB 181 CAGGCAAAACCTGGCCAGGCTCCAGGCTCCATCATATGTCGATCCACAGGGCACT 240  
QY 241 GGCATCCAGACAGGTTCAAGTGGGTCCGGGACAGACTTCACTCTCAACATCACT 300  
DB 241 GGCATCCAGACAGGTTCAAGTGGGTCCGGGACAGACTTCACTCTCAACATCACT 300  
QY 301 AAGCTGAGGCTGAGAGATTTTGCAGTGTATTAATCTGACAGATGATGTTAGTCACTCAG 360  
DB 301 AAGCTGAGGCTGAGAGATTTTGCAGTGTATTAATCTGACAGATGATGTTAGTCACTCAG 360  
QY 361 ACACCTCAGATCACTTCCGCGGAGGAGCAAGGTGAGATCAAAAGAACTGTGGTGA 420  
DB 361 ACACCTCAGATCACTTCCGCGGAGGAGCAAGGTGAGATCAAAAGAACTGTGGTGA 420  
QY 421 CCATCTGTCTGCGCGGTGGCGTTCCGAGAGTGTGATCAAGTGGAGTGGCTCCAG 480  
DB 421 CCATCTGTCTGCGCGGTGGCGTTCCGAGAGTGTGATCAAGTGGAGTGGCTCCAG 480  
QY 481 GTGCACTGTGAGATCTGGGGGAGGCGGTGTCACGCTGGAGGCTCCCTGAGACTCTCC 540  
DB 481 GTGCACTGTGAGATCTGGGGGAGGCGGTGTCACGCTGGAGGCTCCCTGAGACTCTCC 540  
QY 541 TGTGACGCTCTGAGATTCCTTCAGAGCTTTGATGATCACTGGGTCCGCAAGGCTCA 600  
DB 541 TGTGACGCTCTGAGATTCCTTCAGAGCTTTGATGATCACTGGGTCCGCAAGGCTCA 600  
QY 601 GGCAGAGGCGCTGAGTGGGTGAGTATATATATATGATGAGAGCACTAAATATCAAGCA 660  
DB 601 GGCAGAGGCGCTGAGTGGGTGAGTATATATATATATGATGAGAGCACTAAATATCAAGCA 660  
QY 661 GACTCCGTGAAGGCGGATTCACCATCTCCAGAGACACTTCCAGAAACGGGTATCTTA 720  
DB 661 GACTCCGTGAAGGCGGATTCACCATCTCCAGAGACACTTCCAGAAACGGGTATCTTA 720

QY 721 AAATGAACAGCCTGAGAACTGAGGACACGGCTGTCTTACTGTGCGAGATCAGAGC 780  
DB 721 AAATGAACAGCCTGAGAACTGAGGACACGGCTGTCTTACTGTGCGAGATCAGAGC 780  
QY 781 CTGTTGGGTGACTATGACCACTACTACGATTTGACGTCGCGGCAAGGAGCACCGTTC 840  
DB 781 CTGTTGGGTGACTATGACCACTACTACGATTTGACGTCGCGGCAAGGAGCACCGTTC 840  
QY 841 ACCGTCCTCTCAGATCCGAAACAACTGATCAGCGAAGAAATCTGTAACATCAACAT 900  
DB 841 ACCGTCCTCTCAGATCCGAAACAACTGATCAGCGAAGAAATCTGTAACATCAACAT 900  
QY 901 CACCATTTAGTGAAGCTT 918  
DB 901 CACCATTTAGTGAAGCTT 918

#### RESULT 4

AD052295  
ID AD052295 standard; DNA, 918 BP.

XX AC AD052295;

XX DT 29-JUL-2004 (first entry)

XX DE Human antibody H11 scFv DNA #1.

XX KW Antigen binding fragment; H chain V region; L chain V region; C-antigen;

XX KW neoplasia; cancer; vaccine; gene therapy; human;

XX KW single chain V region fragment; scFv; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 1..918

FT FT /tag= a

FT FT /product= "Human antibody H11 scFv protein"

FT FT /transl\_except= (pos:904..915, aa:Hls-Lys)

FT FT /partial

FT FT /note= "No start and stop codon"

XX US2004091484-A1.

XX PN 13-MAY-2004.

XX PF 29-AUG-2003; 2003US-00651453.

XX PR 22-MAY-1996; 96US-00657449.

XX PR 22-MAY-1997; 97US-00862124.

XX PR 13-FEB-2001; 2001US-00782397.

XX PA (DANM/) DAN M D.

XX PA (MAIT/) MAITI P K.

XX PA (KAPL/) KAPLAN H A.

XX PA (GRAD/) GRAD C.

XX PI Dan MD, Maici PK, Kaplan HA, Grad C;

XX DR WPI; 2004-399136/37.

XX DR P-PSDB; AD052296.

XX PT Composition useful for treating neoplasia in patient, comprises antigen  
XX PT binding fragment of antibody specifically recognizing C-antigen  
XX PT recognized by antibody comprising H chain V region and L chain V region.  
XX PS Example 7; SEQ ID NO 13; 56bp; English.

XX CC The invention relates to a composition comprising an antigen binding  
XX CC fragment of an antibody comprising H chain V region and L chain V region  
XX CC treating a patient with a neoplasia. The antigen binding fragment of the  
XX CC antibody is used as diagnostic and imaging reagents. The invention is  
XX CC useful for genetically altering cells in vivo, to treat various types of

CC cancer. It is also useful in vaccine and gene therapy. The present  
 CC sequence is human antibody H11 single chain V region fragment (scFv) DNA.  
 XX  
 SQ Sequence 918 BP; 213 A; 240 C; 264 G; 201 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 12; Length 918;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-227;  
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GAATTCATGAAAAAACCCTATCGCATGCGATGTCAGTGGCTGGTTCCGTACCGTT 60
DB 1 GAATTCATGAAAAAACCCTATCGCATGCGATGTCAGTGGCTGGTTCCGTACCGTT 60
QY 61 GCGCAGGCGCGATATTGTGTGACGAGTCCAGGACCCCTGCTTGTCTCCAGGGGAA 120
DB 61 GCGCAGGCGCGATATTGTGTGACGAGTCCAGGACCCCTGCTTGTCTCCAGGGGAA 120
QY 121 AGAGCCACCCTCTCTGCGAGGGCCAGTCAAGTGTAGTACAGTACTTACCTGGTAC 180
DB 121 AGAGCCACCCTCTCTGCGAGGGCCAGTCAAGTGTAGTACAGTACTTACCTGGTAC 180
QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGCGCACT 240
DB 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGCGCACT 240
QY 241 GGCATGCCAGAGGTTCAAGTGGGTCGGGACAGACTTCACTCTCAACATCACT 300
DB 241 GGCATGCCAGAGGTTCAAGTGGGTCGGGACAGACTTCACTCTCAACATCACT 300
QY 301 AGACTGAGACCTGAGATTGTCAGTGTATTACTGTCAAGATGATGATGATGATGAT 360
DB 301 AGACTGAGACCTGAGATTGTCAGTGTATTACTGTCAAGATGATGATGATGATGAT 360
QY 361 ACACCTCAGATCACTTTCGCGAGGAGCAAGTGGAGATCAAAAGCACTGTGCTGCA 420
DB 361 ACACCTCAGATCACTTTCGCGAGGAGCAAGTGGAGATCAAAAGCACTGTGCTGCA 420
QY 421 CCATCTGTCTCGCGGTGGCGGTCCTCGAGGTGTGATCAAGTGGAGTGGTCCGAG 480
DB 421 CCATCTGTCTCGCGGTGGCGGTCCTCGAGGTGTGATCAAGTGGAGTGGTCCGAG 480
QY 481 GTGCACTGTGTGAGTCTGGGGAGGCGTGTTCAGGCTGGGAGGTCCTGAGACTTCC 540
DB 481 GTGCACTGTGTGAGTCTGGGGAGGCGTGTTCAGGCTGGGAGGTCCTGAGACTTCC 540
QY 541 TGTGAGGCTCTGAGATTCCTCTTCAAGACCTTGTGATGCACTGGGTCCGAGGCTCT 600
DB 541 TGTGAGGCTCTGAGATTCCTCTTCAAGACCTTGTGATGCACTGGGTCCGAGGCTCT 600
QY 601 GGCAGAGGCGTGTGAGTGGTGGCAGTATATCATATGATGAAAGCACTAAATCAACGA 660
DB 601 GGCAGAGGCGTGTGAGTGGTGGCAGTATATCATATGATGAAAGCACTAAATCAACGA 660
QY 661 GACTCCGTGAAAGGCGGATTCACATCTCCAGAGACCTTCCAGAGAACGCTGTATCTA 720
DB 661 GACTCCGTGAAAGGCGGATTCACATCTCCAGAGACCTTCCAGAGAACGCTGTATCTA 720
QY 721 AAATGAAACAGCTGAGAACTGAGAACAGGCTGTCTATTACTGTGCGAGATGAGAGC 780
DB 721 AAATGAAACAGCTGAGAACTGAGAACAGGCTGTCTATTACTGTGCGAGATGAGAGC 780
QY 781 CTGTGGGTGACTATGACCACTAAGTGTGACGTCTGGGGCAAGAGGACCAAGGTC 840
DB 781 CTGTGGGTGACTATGACCACTAAGTGTGACGTCTGGGGCAAGAGGACCAAGGTC 840
QY 841 ACCGCTCTCCTCAGATCCGAAACAAAATGATCAAGGAAAGATCTGAACATCAACAT 900
DB 841 ACCGCTCTCCTCAGATCCGAAACAAAATGATCAAGGAAAGATCTGAACATCAACAT 900
QY 901 CACCATTAAGTGAAGCTT 918
DB 901 CACCATTAAGTGAAGCTT 918

```

RESULT 5  
 AAD04538/c  
 ID AAD04538 standard; DNA; 918 BP.

AC AAD04538;  
 XX  
 DT 04-UTL-2001 (first entry)

DE Human H11-single chain variable region (scFv) complementary DNA #1.  
 XX  
 XX Human; monoclonal antibody; Mab; H11; single chain variable region; scFv;  
 KW neoplastic disease; melanoma; immunoglobulin IGM; gene therapy; lymphoma;  
 KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;  
 KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;  
 KW C-antigen; chronic leukemia; glioma; ds.

OS Homo sapiens.  
 XX  
 PN US6207153-B1.

PD 27-MAR-2001.  
 XX  
 PF 22-MAY-1997; 97US-00862124.

PR 22-MAY-1996; 96US-00657449.  
 XX  
 PA (VIVE-) VIVENTIA BIOTECH INC.

PI Dan MD, Maitl PK, Kaplan HA;  
 XX  
 DR WPI, 2001-289584/30.

PT Composition comprising antigen binding fragments of an antibody that  
 PT recognizes an antigen on neoplastic cells but not on normal cells for use  
 PT in diagnosis, imaging and treatment of carcinomas.  
 XX  
 XX Example 7; Col 65-66; 56pp; English.

PS The present sequence is human monoclonal antibody (Mab), H11-single chain  
 CC variable region (scFv) complementary DNA. The invention relates to human  
 CC monoclonal antibody (Mab) H11, H11-(scFv) single chain variable (V)  
 CC region fragment and their corresponding DNA molecules. H11 antibody is an  
 CC immunoglobulin of IGM subclass which is specific to C-antigen found  
 CC specifically on neoplastic cells and not on normal cells. H11 is an  
 CC antibody obtained from the fusion of peripheral blood lymphocytes of a 64  
 CC year old male with a low grade glioma and fused to a human myeloma cell  
 CC line to produce a hybridoma designated NBGM/H11. A pharmaceutical  
 CC composition comprising H11 and its derivatives are useful in the  
 CC diagnosis, imaging and treatment of neoplastic disease, particularly,  
 CC melanoma, breast carcinoma, lung carcinoma, ovarian carcinoma, colon  
 CC carcinoma, gastric carcinoma, prostate carcinoma, lymphoma carcinoma,  
 CC neuroblastoma, glioma, soft tissue sarcoma, small cell lung carcinoma,  
 CC prostatic adenocarcinoma, B and T cell lymphomas and chronic leukemias.  
 CC H11 DNA is also used in vaccines and gene therapy

XX  
 SQ Sequence 918 BP; 201 A; 265 C; 239 G; 213 T; 0 U; 0 Other;

Query Match 99.8%; Score 916.4; DB 4; Length 918;  
 Best Local Similarity 99.9%; Pred. No. 4.6e-227;  
 Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 GAATTCATGAAAAAACCCTATCGCATGCGATGTCAGTGGCTGGTTCCGTACCGTT 60
DB 1 GAATTCATGAAAAAACCCTATCGCATGCGATGTCAGTGGCTGGTTCCGTACCGTT 60
QY 61 GCGCAGGCGCGATATTGTGTGACGAGTCCAGGACCCCTGCTTGTCTCCAGGGGAA 120
DB 61 GCGCAGGCGCGATATTGTGTGACGAGTCCAGGACCCCTGCTTGTCTCCAGGGGAA 120
QY 121 AGAGCCACCCTCTCTGCGAGGGCCAGTCAAGTGTAGTACAGTACTTACCTGGTAC 180
DB 121 AGAGCCACCCTCTCTGCGAGGGCCAGTCAAGTGTAGTACAGTACTTACCTGGTAC 180
QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGCGCACT 240
DB 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGCGCACT 240
QY 241 GGCATGCCAGAGGTTCAAGTGGGTCGGGACAGACTTCACTCTCAACATCACT 300
DB 241 GGCATGCCAGAGGTTCAAGTGGGTCGGGACAGACTTCACTCTCAACATCACT 300
QY 301 AGACTGAGACCTGAGATTGTCAGTGTATTACTGTCAAGATGATGATGATGATGAT 360
DB 301 AGACTGAGACCTGAGATTGTCAGTGTATTACTGTCAAGATGATGATGATGATGAT 360
QY 361 ACACCTCAGATCACTTTCGCGAGGAGCAAGTGGAGATCAAAAGCACTGTGCTGCA 420
DB 361 ACACCTCAGATCACTTTCGCGAGGAGCAAGTGGAGATCAAAAGCACTGTGCTGCA 420
QY 421 CCATCTGTCTCGCGGTGGCGGTCCTCGAGGTGTGATCAAGTGGAGTGGTCCGAG 480
DB 421 CCATCTGTCTCGCGGTGGCGGTCCTCGAGGTGTGATCAAGTGGAGTGGTCCGAG 480
QY 481 GTGCACTGTGTGAGTCTGGGGAGGCGTGTTCAGGCTGGGAGGTCCTGAGACTTCC 540
DB 481 GTGCACTGTGTGAGTCTGGGGAGGCGTGTTCAGGCTGGGAGGTCCTGAGACTTCC 540
QY 541 TGTGAGGCTCTGAGATTCCTCTTCAAGACCTTGTGATGCACTGGGTCCGAGGCTCT 600
DB 541 TGTGAGGCTCTGAGATTCCTCTTCAAGACCTTGTGATGCACTGGGTCCGAGGCTCT 600
QY 601 GGCAGAGGCGTGTGAGTGGTGGCAGTATATCATATGATGAAAGCACTAAATCAACGA 660
DB 601 GGCAGAGGCGTGTGAGTGGTGGCAGTATATCATATGATGAAAGCACTAAATCAACGA 660
QY 661 GACTCCGTGAAAGGCGGATTCACATCTCCAGAGACCTTCCAGAGAACGCTGTATCTA 720
DB 661 GACTCCGTGAAAGGCGGATTCACATCTCCAGAGACCTTCCAGAGAACGCTGTATCTA 720
QY 721 AAATGAAACAGCTGAGAACTGAGAACAGGCTGTCTATTACTGTGCGAGATGAGAGC 780
DB 721 AAATGAAACAGCTGAGAACTGAGAACAGGCTGTCTATTACTGTGCGAGATGAGAGC 780
QY 781 CTGTGGGTGACTATGACCACTAAGTGTGACGTCTGGGGCAAGAGGACCAAGGTC 840
DB 781 CTGTGGGTGACTATGACCACTAAGTGTGACGTCTGGGGCAAGAGGACCAAGGTC 840
QY 841 ACCGCTCTCCTCAGATCCGAAACAAAATGATCAAGGAAAGATCTGAACATCAACAT 900
DB 841 ACCGCTCTCCTCAGATCCGAAACAAAATGATCAAGGAAAGATCTGAACATCAACAT 900
QY 901 CACCATTAAGTGAAGCTT 918
DB 901 CACCATTAAGTGAAGCTT 918

```

QY 181 CAGCAGAAACCTGGCCAGGCTCCCAAGCTCTCATCTATGTGTCATCCACAGGCTCACT 240  
DB 738 CAGCAGAAACCTGGCCAGGCTCCCAAGCTCTCATCTATGTGTCATCCACAGGCTCACT 679  
QY 241 GGCATGCCAGACAGGTTTCAGTGCAGTGGGTCCGGGACAGACTTCACTCCACCACT 300  
DB 678 GGCATGCCAGACAGGTTTCAGTGCAGTGGGTCCGGGACAGACTTCACTCCACCACT 619  
QY 301 AGACTGAGCCTGGAAGATTTTTCAGTGTATTACTGTCAAGATGATGATCACTCCAG 360  
DB 618 AGACTGAGCCTGGAAGATTTTTCAGTGTATTACTGTCAAGATGATGATCACTCCAG 559  
QY 361 ACACCTCAGATCACTTTCGCGGAGGACCAAGGTGAGATCAAACTGTGGCTGCA 420  
DB 558 ACACCTCAGATCACTTTCGCGGAGGACCAAGGTGAGATCAAACTGTGGCTGCA 499  
QY 421 CCATCTGTCTCGCGGTGGCGGTTCGAGAGGTGAGATCAAGTGGAGGTGCTCCAG 480  
DB 498 CCATCTGTCTCGCGGTGGCGGTTCGAGAGGTGAGATCAAGTGGAGGTGCTCCAG 439  
QY 481 GTGCACTGTGAGTCTGCGGAGGCGTGTCTCAGCTGGAGTCCCTGAGACTCTCC 540  
DB 438 GTGCACTGTGAGTCTGCGGAGGCGTGTCTCAGCTGGAGTCCCTGAGACTCTCC 379  
QY 541 TGTGACGCTCTGAGATTTCCCTTCAGAAAGCTTGTGATGACCTGGGTCCGCGCTCTA 600  
DB 378 TGTGACGCTCTGAGATTTCCCTTCAGAAAGCTTGTGATGACCTGGGTCCGCGCTCTA 319  
QY 601 GGCAGAGGCTGAGAGTGGGTGGAGTATATCATATGATGAGAGCTAAATCTACGCA 660  
DB 318 GGCAGAGGCTGAGAGTGGGTGGAGTATATCATATGATGAGAGCTAAATCTACGCA 259  
QY 661 GACTCCGTGAAAGGCGGATTCACCATCTCCAGAGACACTTCCAAAGACAGGCTGATCTA 720  
DB 258 GACTCCGTGAAAGGCGGATTCACCATCTCCAGAGACACTTCCAAAGACAGGCTGATCTA 199  
QY 721 AAAATGAACAGCTTGAAGATGAGACAGGCTGTCTATTAATCTGTGAGAGATCAAGC 780  
DB 198 AAAATGAACAGCTTGAAGATGAGACAGGCTGTCTATTAATCTGTGAGAGATCAAGC 139  
QY 781 CTTGTGGTGAATGATCACTACTACGTTTGGAGTCTGGGGCAAGGGACACAGGTC 840  
DB 138 CTTGTGGTGAATGATCACTACTACGTTTGGAGTCTGGGGCAAGGGACACAGGTC 79  
QY 841 ACCGTCTCTCAGAGATCCGAAACAAAACCTGATCAGGAGAGATCTGAACCATCACT 900  
DB 78 ACCGTCTCTCAGAGATCCGAAACAAAACCTGATCAGGAGAGATCTGAACCATCACT 19  
QY 901 CACCATTTAGTGAAGCTT 918  
DB 18 CACCATTTAGTGAAGCTT 1

RESULT 6  
AD052297/c  
ID AD052297 standard; DNA; 918 BP.  
XX  
AC AD052297;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human antibody H11 scFv complementary DNA #1.  
XX  
KM Antigen binding fragment; H chain V region; L chain V region; C-antigen;  
XX neoplasia; cancer; vaccine; gene therapy; human;  
XX single chain V region fragment; scFv; gene; de.  
OS Homo sapiens.  
XX  
XX US2004091484-A1.  
PN  
XX  
PD 13-MAY-2004.

XX 29-AUG-2003; 2003US-00651453.  
PF 22-MAY-1996; 96US-00657449.  
PR 22-MAY-1997; 97US-00862124.  
PR 13-FEB-2001; 2001US-00782397.  
XX  
PA (DANM/) DAN M D.  
PA (WALT/) WALT P K.  
PA (KAPL/) KAPLAN H A.  
PA (GRAD/) GRAD C.  
PI Dan MD, Maiti PK, Kaplan HA, Grad C;  
XX WPI; 2004-399136/37.  
DR  
XX  
PT Composition useful for treating neoplasia in patient, comprises antigen  
PT binding fragment of antibody specifically recognizing C-antigen  
PT recognized by antibody comprising H chain V region and L chain V region.  
XX  
PS Example 7; SEQ ID NO 15; 56pp; English.  
XX  
CC The invention relates to a composition comprising an antigen binding  
CC fragment of an antibody comprising H chain V region and L chain V region  
CC that specifically recognises C-antigen. The invention is useful for  
CC treating a patient with a neoplasia. The antigen binding fragment of the  
CC antibody is used as diagnostic and imaging reagents. The invention is  
CC useful for genetically altering cells in vivo, to treat various types of  
CC cancer. It is also useful in vaccine and gene therapy. The present  
CC sequence is human antibody H11 single chain V region fragment (scFv)  
CC complementary DNA.  
XX  
SQ Sequence 918 BP; 201 A; 265 C; 239 G; 213 T; 0 U; 0 Other;  
XX  
Query Match 99.8%; Score 916.4; DB 12; Length 918;  
Best Local Similarity 99.9%; Pred. No. 4.6e-227;  
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GAATTCATGAAAAAACCCTATCCGATCGAGTTCGACTGGCTGCTACCGTT 60  
DB 918 GAATTCATGAAAAAACCCTATCCGATCGAGTTCGACTGGCTGCTACCGTT 859  
QY 61 GGCAGAGCCGATTTGTTGACGAGTCTCCAGAGCCTCTTGTCTCCAGGGGAA 120  
DB 858 GGCAGAGCCGATTTGTTGACGAGTCTCCAGAGCCTCTTGTCTCCAGGGGAA 799  
QY 121 AGAGCACCCTCTCTCGAGGGCCAGTCAAGTGTATGACAGCTTACCTTACCTGATC 180  
DB 798 AGAGCACCCTCTCTCGAGGGCCAGTCAAGTGTATGACAGCTTACCTTACCTGATC 739  
QY 181 CAGCAGAAACCTGGCCAGGCTCCCAAGCTCTCATCTATGTGTCATCCACAGGCTCACT 240  
DB 738 CAGCAGAAACCTGGCCAGGCTCCCAAGCTCTCATCTATGTGTCATCCACAGGCTCACT 679  
QY 241 GGCATGCCAGACAGTTCAGTGCAGTGGGTCCGGGACAGACTTCACTCCACCACT 300  
DB 678 GGCATGCCAGACAGTTCAGTGCAGTGGGTCCGGGACAGACTTCACTCCACCACT 619  
QY 301 AGACTGAGCCTGGAAGATTTTTCAGTGTATTACTGTCAAGATGATGATCACTCCAG 360  
DB 618 AGACTGAGCCTGGAAGATTTTTCAGTGTATTACTGTCAAGATGATGATCACTCCAG 559  
QY 361 ACACCTCAGATCACTTTCGCGGAGGACCAAGGTGAGATCAAACTGTGGCTGCA 420  
DB 558 ACACCTCAGATCACTTTCGCGGAGGACCAAGGTGAGATCAAACTGTGGCTGCA 499  
QY 421 CCATCTGTCTCGCGGTGGCGGTTCGAGAGGTGAGATCAAGTGGAGGTGCTCCAG 480  
DB 498 CCATCTGTCTCGCGGTGGCGGTTCGAGAGGTGAGATCAAGTGGAGGTGCTCCAG 439  
QY 481 GTGCACTGTGAGTCTGCGGAGGCGTGTCTCAGCTGGAGTCCCTGAGACTCTCC 540  
DB 438 GTGCACTGTGAGTCTGCGGAGGCGTGTCTCAGCTGGAGTCCCTGAGACTCTCC 379



```

QY 541 TGTGAGGCGCTGGATTCCCTTCCAGAGCTTGTATGACATGGGTCGGCAGGCTCTA 600
DB 378 TGTGAGGCTTGGATTCCCTTCCAGAGCTTGTATGACATGGGTCGGCAGGCTCTA 319
QY 601 GGCAGAGGGCTGGAGTGGTGGCAGTTATATCATATGATGAAGCACTAAATCTACGCA 660
DB 318 GGCAGAGGGCTGGAGTGGTGGCAGTTATATCATATGATGAAGCACTAAATCTACGCA 259
QY 661 GACTCCGTGAAGGGCCGATTACCATCTCCAGAGCACTTCCAGAAACGGGTATCTA 720
DB 258 GACTCCGTGAAGGGCCGATTACCATCTCCAGAGCACTTCCAGAAACGGGTATCTA 199
QY 721 AAAATGAAGAGCTGGAATGAGACAGGCGTGTATATCTGTCTGAGAGATCTAGAGC 780
DB 198 AAAATGAAGAGCTGGAATGAGACAGGCGTGTATATCTGTCTGAGAGATCTAGAGC 139
QY 781 CTGTTGGGTGACTATGACCACTACTACGGTTTGAAGCTGAGGGCAAGGACCAAGCTC 840
DB 138 CTGTTGGGTGACTATGACCACTACTACGGTTTGAAGCTGAGGGCAAGGACCAAGCTC 79
QY 841 ACCGTCCTCAGAGATCCGAAACAAACTGATCAGCGAAAGATCTGAACCATCACAT 900
DB 78 ACCGTCCTCAGAGATCCGAAACAAACTGATCAGCGAAAGATCTGAACCATCACAT 19
QY 901 CACCATTAAGTGAAGCTT 918
DB 18 CACCATTAAGTGAAGCTT 1

```

```

RESULT 7
AAV10119
ID AAV10119 standard; DNA; 867 BP.
XX
XX AAV10119;
DT 29-MAY-1998 (first entry)
XX
DE Human H11-scFv construct dimer forming DNA sequence.
XX
XX H11, monoclonal antibody; Mab; C-antigen; variable region heavy chain;
KW V region; H chain; neoplasia; detection; lymphoma; tumor cell; probe;
KW primer; vaccine; gene therapy; glioblastoma; neuroblastoma;
KW malignant melanoma; adenocarcinoma; small cell lung carcinoma;
KW single chain variable region; scFv; ss.
OS Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 1..867
FT FT /*tag= a
FT FT /product= "H11-scFv construct"
FT FT /note= "partial sequence of dimer forming construct is
FT FT interrupted by an intron."
FT FT 856..861
FT FT /*tag= b
XX
XX WO9744461-A2.
XX
XX 27-NOV-1997.
XX
XX 22-MAY-1997; 97WO-US008962.
XX
XX 22-MAY-1996; 96US-00657449.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Dan MD, Malet PK, Kaplan HA,
XX
XX WPI, 1998-018515/02.
XX
XX P-PSDB; AAW40071.
XX

```

```

PT Antigen binding fragment from monoclonal antibody, H11 - allows tumour
PT specific detection and treatment of neoplasia.
XX
XX Example 7; Page 94-95; 126pp; English.
XX
CC This sequence encodes a human H11 monoclonal antibody single chain V
CC region fragment (H11-scFv) construct which is capable of forming dimers.
CC This construct is used to determine the ability of H11-scFv antibody
CC fragments to bind specifically to the C-antigen on cancer cells. Such
CC antigen binding fragments may be used for treating a patient with
CC neoplasia. It is especially useful in the detection of lymphomas and
CC leukemias where the tumour cells bearing the C antigen are circulating
CC in the patients bloodstream. The polynucleotide sequence may be used as a
CC primer or a probe and the encoded protein may be used in a vaccine or for
CC gene therapy. The human monoclonal antibody (Mab), designated H11,
CC specifically recognises cancerous cells. H11 is specific for
CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,
CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
CC prostate adenocarcinoma
XX
SQ Sequence 867 BP; 209 A; 229 C; 241 G; 188 T; 0 U; 0 Other;
Query Match 87.1%; Score 799.6; DB 2; Length 867;
Best Local Similarity 94.0%; Pred No. 7.9e-197;
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;
QY 1 GAATTCATGAAAAAAACCGCTATCCGATGAGATTGCACTGGCTGGTTCCGTAACGTT 60
DB 1 GAATTCATGAAAAAAACCGCTATCCGATGAGATTGCACTGGCTGGTTCCGTAACGTT 60
QY 61 GCGCAGGCGGATATGTGTGTGACGAGTCTCCAGAGCACTCTTTGTCTCCAGGGAAA 120
DB 61 GCGCAGGCGGATATGTGTGTGACGAGTCTCCAGAGCACTCTTTGTCTCCAGGGAAA 120
QY 121 AGAGCCACCCCTCTCCGTCAGAGGCGAGTCAGAGTGTAGAGAGCTTAAAGCGGTGAC 180
DB 121 AGAGCCACCCCTCTCTGACGGGCGACTCAGAGTGTAGAGAGCTTAAAGCGGTGAC 180
QY 181 CAGCAAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGTGATCCACAGGGCCACT 240
DB 181 CAGCAAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGTGATCCACAGGGCCACT 240
QY 241 GGCATGCCAGACAGATTCTGAGTGGAGTGGGTCCGGACAGACTTCACTTCAACATCAGT 300
DB 241 GGCATGCCAGACAGATTCTGAGTGGAGTGGGTCCGGACAGACTTCACTTCAACATCAGT 300
QY 301 AGACTGAGGCGTGAAGATTTTGCAGTGTATTACTGTCCAGCAGTATGATGCTCAGCTCAG 360
DB 301 AGACTGAGGCGTGAAGATTTTGCAGTGTATTACTGTCCAGCAGTATGATGCTCAGCTCAG 360
QY 361 ACACCTCAGATCACTTTCCGCGAGAGGACCAAGTGTGAGATCAAAAGAACTGTGCTGCA 420
DB 361 ACACCTCAGATCACTTTCCGCGAGAGGACCAAGTGTGAGATCAAAAGAACTGTGCTGCA 420
QY 421 CCATCTGTCTCTGGCGGTGGCGGTTCCGAGGTGTGATCAGTGTGAGGTGCTCCAG 480
DB 421 TC-----CGGACAG 429
QY 481 GTGCAAGCTGTGAGTGTGGGGAGGCGGTGTCAGGCTGGAGAGTCCCTGAGACTCTCC 540
DB 481 GTGCAAGCTGTGAGTGTGGGGAGGCGGTGTCAGGCTGGAGAGTCCCTGAGACTCTCC 540
QY 490 GTGCAAGCTGTGAGTGTGGGGAGGCGGTGTCAGGCTGGAGAGTCCCTGAGACTCTCC 489
DB 490 GTGCAAGCTGTGAGTGTGGGGAGGCGGTGTCAGGCTGGAGAGTCCCTGAGACTCTCC 489
QY 541 TGTGAGGCTCTGATTCCTTCCAGAACTTGTGTATGACATGGGTCCGCGAGGCTCTA 600
DB 541 TGTGAGGCTCTGATTCCTTCCAGAACTTGTGTATGACATGGGTCCGCGAGGCTCTA 600
QY 601 GGCAGAGGGCTGGAGTGGTGGCAGTTATATCATATGATGAAGCACTAAATCTACGCA 660
DB 601 GGCAGAGGGCTGGAGTGGTGGCAGTTATATCATATGATGAAGCACTAAATCTACGCA 660
QY 661 GACTCCGTGAAGGGCCGATTACCATCTCCAGAGCACTTCCAGAAACGGGTATCTA 720
DB 661 GACTCCGTGAAGGGCCGATTACCATCTCCAGAGCACTTCCAGAAACGGGTATCTA 720
QY 721 AAAATGAAGAGCTGGAATGAGACAGGCGTGTATATCTGTCTGAGAGATCTAGAGC 780
DB 721 AAAATGAAGAGCTGGAATGAGACAGGCGTGTATATCTGTCTGAGAGATCTAGAGC 780

```

QY 721 AAATGAACAGCCTGAGAACTGAGACACGCGTCTCTATTACTGTGCGAGATCAGAGC 780  
 Db 670 AAATGAACAGCCTGAGAACTGAGACACGCGTCTCTATTACTGTGCGAGATCAGAGC 729  
 QY 781 CTTGTTGGGAGCTATATACCACTCTACGTTTGGAGCTCGGGGCAAAAGGACCAAGGTC 840  
 Db 730 CTTGTTGGGAGCTATATACCACTCTACGTTTGGAGCTCGGGGCAAAAGGACCAAGGTC 789  
 QY 841 ACCGTCCTCAGATCCGAAACAACTGATCAGCGAAGAGATCTGAACCATCACCAT 900  
 Db 790 ACCGTCCTCAGATCCGAAACAACTGATCAGCGAAGAGATCTGAACCATCACCAT 849  
 QY 901 CACCATTAAGTGAAGCTT 918  
 Db 850 CACCATTAAGTGAAGCTT 867

RESULT 8  
 AAD04539 standard; DNA; 867 BP.  
 XX AAD04539;  
 AC AAD04539;  
 DT 04-JUL-2001 (first entry)  
 XX  
 DE Human monoclonal antibody H11-single chain variable region (scFv) DNA #2.  
 XX  
 KW Human; monoclonal antibody; Mab; H11; single chain variable region; scFv;  
 KW neoplastic disease; melanoma; immunoglobulin Igm; gene therapy; lymphoma;  
 KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;  
 KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;  
 KW C-antigen; chronic leukaemia; glioma; ds.  
 XX

OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..867  
 FT /tag= a  
 FT /product= "Human H11-single chain variable region (scFv)"  
 FT /transl\_except= (pos:853..864, aa:Hls-Lys)  
 FT /note= "Insertion of two inframe stop codon alters the  
 FT reading frame; CDS does not include start and stop  
 FT codons"  
 FT /partial

US6207153-B1.  
 PN 27-MAR-2001.  
 PD 22-MAY-1997; 97US-00862124.  
 PF 22-MAY-1996; 96US-00657449.  
 PR (VIVE-) VIVENTIA BIOTECH INC.  
 PA Dan MD, Maiti PK, Kaplan HA;  
 PI WPI; 2001-289584/30.  
 DR P-PSDB; AAB00948.  
 DR  
 DR Composition comprising antigen binding fragments of an antibody that  
 PT recognizes an antigen on neoplastic cells but not on normal cells for use  
 PT in diagnosis, imaging and treatment of carcinomas.  
 XX  
 PS Example 7; Col 67-70; 56pp; English.  
 XX  
 CC The present DNA sequence encodes human monoclonal antibody (Mab), H11-  
 CC single chain variable region (scFv). The H11 light chain variable region  
 CC is linked to the heavy chain variable region through a (SGGGS)3 linker to  
 CC form dimers. The invention relates to human monoclonal antibody (Mab)  
 CC H11, H11-(scFv) single chain variable (V) region fragment and their  
 CC corresponding DNA molecules. H11 antibody is an immunoglobulin of Igm

CC subclass which is specific to C-antigen found specifically on neoplastic  
 CC cells and not on normal cells. H11 is an antibody obtained from the  
 CC fusion of peripheral blood lymphocytes of a 64 year old male with a low  
 CC grade glioma and fused to a human myeloma cell line to produce a  
 CC hybridoma designated NB6M1/H11. A pharmaceutical composition comprising  
 CC H11 and its derivatives are useful in the diagnosis, imaging and  
 CC treatment of neoplastic disease, particularly, melanoma, breast  
 CC carcinoma, lung carcinoma, ovarian carcinoma, colon carcinoma, gastric  
 CC carcinoma, prostate carcinoma, lymphoma carcinoma, neuroblastoma, glioma,  
 CC soft tissue sarcoma, small cell lung carcinoma, prostatic adenocarcinoma,  
 CC B and T cell lymphomas and chronic leukaemias. H11 DNA is also used in  
 CC vaccines and gene therapy  
 XX

SO Sequence 867 BP; 209 A; 229 C; 241 G; 188 T; 0 U; 0 Other;  
 Query Match 87.1%; Score 799.6; DB 4; Length 867;  
 Best Local Similarity 94.0%; Pred. No. 7.9e-197;  
 Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

QY 1 GAATTCATGAAAAAACCCTATCCGATCGAGTTCAGTGGCTGGTTCGCTACCGTT 60  
 Db 1 GAATTCATGAAAAAACCCTATCCGATCGAGTTCAGTGGCTGGTTCGCTACCGTT 60  
 QY 61 GCGCAGGCCGATATGTTGTTGACGAGTCTCAGAGCACCCTGTCTTGTCTCCAGGGAA 120  
 Db 61 GCGCAGGCCGATATGTTGTTGACGAGTCTCAGAGCACCCTGTCTTGTCTCCAGGGAA 120  
 QY 121 AGAGCCACCTCTCTCCGACGGGCGACATCAGAGTTTAAAGACATCTAGCTCGGTAC 180  
 Db 121 AGAGCCACCTCTCTCCGACGGGCGACATCAGAGTTTAAAGACATCTAGCTCGGTAC 180  
 QY 181 CAGCAGAAACCTGGGCGAGGCTCCAGGCTCTCATCTATGATGATCAGCAGGCGCACT 240  
 Db 181 CAGCAGAAACCTGGGCGAGGCTCCAGGCTCTCATCTATGATGATCAGCAGGCGCACT 240  
 QY 241 GGCATGCCAGACAGGTTCAAGTGGCAGTGGTCCGGGACAGACTTCACTCACCATCAGT 300  
 Db 241 GGCATGCCAGACAGGTTCAAGTGGCAGTGGTCCGGGACAGACTTCACTCACCATCAGT 300  
 QY 301 AGACTGGAGCTGAAATTTTGAAGTATTAATCTGTCAGAGATGATGATGATGATGATG 360  
 Db 301 AGACTGGAGCTGAAATTTTGAAGTATTAATCTGTCAGAGATGATGATGATGATGATG 360  
 QY 361 ACACCTCAGATCACTTTCGCGGAGGACCAAGTGAAGTCAAGAACTGTGGCTGCA 420  
 Db 361 ACACCTCAGATCACTTTCGCGGAGGACCAAGTGAAGTCAAGAACTGTGGCTGCA 420  
 QY 421 CCATCTGTCTTGGCGGTGGCGGTTCCGAGGTGTGATCAGGTGAGGTGGCTCCAG 480  
 Db 421 TC-----CGACAG 429  
 QY 481 GTGCAGCTGTGATGATCTTGGGGAGGCGTGTCCAGCTGGGAGGTCCTGAGACTTCC 540  
 Db 430 GTGCAGCTGTGATGATCTTGGGGAGGCGTGTCCAGCTGGGAGGTCCTGAGACTTCC 489  
 QY 541 TGTGACGCTTGGATTTCCCTTCAAGAGCTTGTGATGATGATGATGATGATGATGATG 600  
 Db 490 TGTGACGCTTGGATTTCCCTTCAAGAGCTTGTGATGATGATGATGATGATGATGATG 549  
 QY 601 GGCAGAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
 Db 550 GGCAGAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 609  
 QY 661 GACTCCGTGAAGGGCCGATTCACATCTCCAGAGACCTTCCAAAGACAGGGTATCTA 720  
 Db 610 GACTCCGTGAAGGGCCGATTCACATCTCCAGAGACCTTCCAAAGACAGGGTATCTA 669  
 QY 721 AAATGAACAGCCTGAGAACTGAGACACGCGTCTCTATTACTGTGCGAGATCAGAGC 780  
 Db 670 AAATGAACAGCCTGAGAACTGAGACACGCGTCTCTATTACTGTGCGAGATCAGAGC 729  
 QY 781 CTTGTTGGGAGCTATATACCACTCTACGTTTGGAGCTCGGGGCAAAAGGACCAAGGTC 840

Db	730	CTGTTGGGAGCATATACCACTACTACGAGTTTGGAGCTCTGGGGCAAAAGGACCAAGGCTC	789
Qy	841	ACCGTCTCTCCAGAGATCCGAACAAAACTGATCAGCGAGAGAGATCTGAACATCAACCAT	900
Db	790	ACCGTCTCTCCAGAGATCCGAACAAAACTGATCAGCGAGAGAGATCTGAACATCAACCAT	849
Qy	901	CACCATTAAGTGAAGCTT	918
Db	850	CACCATTAAGTGAAGCTT	867
RESULT 9			
ID	ACA62170	standard; DNA; 867 BP.	
AC	ACA62170;		
XX			
DT	07-AUG-2003	(first entry)	
XX			
DE	C-antigen antibody H11 single chain variable region fragment #2 DNA.		
XX			
KW	Human; ds; gene; H11; single chain variable region; gene therapy; scFv;		
KW	neoplasia; tumour; recurrence risk; C-antigen; melanoma; neuroblastoma;		
KW	glioma; soft tissue sarcoma; small cell lung carcinoma; brain cancer;		
KW	C-antigen specific antibody; alphaC; vaccine; cancer.		
XX			
OS	Homo sapiens.		
XX			
OS	Synthetic.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	1..867	
FT		/*tag= a	
FT		/partial	
FT		/product= "H11 single chain variable region fragment #2"	
FT		/transl_except= (pos:853..934,aa:His-Lys)	
FT		/note= "No start or stop codon given"	
XX			
FN	US2003021779-A1.		
XX			
PD	30-JAN-2003.		
XX			
PE	13-FEB-2001; 2001US-00782397.		
XX			
PR	22-MAY-1996;	96US-00657449.	
PR	22-MAY-1997;	97US-00862124.	
XX			
PA	(DANM/) DAN M D.		
PA	(MAIT/) MAIT P K.		
PA	(KAPL/) KAPLAN H A.		
XX			
P1	Dan MD, Maici PK, Kaplan HA;		
XX			
DR	WPI: 2003-456278/43.		
DR	P-PSDB; ABU10487.		
XX			
PT	Novel antigen binding fragment of monoclonal antibody specific for		
PT	cancer detected on neoplastic cells, useful for diagnosing or treating		
PT	cancer, for manufacturing novel reagents and as diagnostic and imaging		
PT	reagent.		
XX			
XX	Example 7; Page 35-36; 62pp; English.		
XX			
CC	The invention relates to a polypeptide which is an antigen binding		
CC	fragment of a monoclonal antibody specific for an antigen detected on		
CC	neoplastic cells. The antigen binding fragment (ABF) is useful for		
CC	treating a patient with a neoplasia. The individual has a clinically		
CC	detectable tumour. The method is useful for palliating the neoplasia. The		
CC	method reduces the risk of recurrence of a clinically detectable tumour.		
CC	The antigen binding fragment is labelled with a therapeutic moiety such		
CC	as radioisotopes or immunomodulators. ABF is useful for detecting C-		
CC	antigen in a sample. The polypeptide is useful for diagnosing, localising		
CC	and/or treating neoplasias, including melanoma, neuroblastoma, glioma,		
CC	soft tissue sarcoma and small cell lung carcinoma. The polypeptide is		

Query Match	87.1%	Score 799.6	DB 9	Length 867
Best Local Similarity	94.0%	Pred. No. 7.9e-197		
Matches	863	Conservative	0	Mismatches 4; Indels 51; Gaps 1
QY 1 GAATTCATGAAAAAACCCGCTATGCGATCCGACGTGCGCTGCTTGGCTACCGTT	60			
Db 1 GAATTCATGAAAAAACCCGCTATGCGATCCGACGTGCGCTGCTTGGCTACCGTT	60			
QY 61 GGGCAGGCGGCAATTTGTTGACGAGCTCCAGGACCCGTCCTTGTCTCCAGGGAA	120			
Db 61 GGGCAGGCGGCAATTTGTTGACGAGCTCCAGGACCCGTCCTTGTCTCCAGGGAA	120			
QY 121 AGAGCCACCTCTCCTCGACGGGCGCAGTCAGAGTGTATTAGACGATCTTAAGCTGTATC	180			
Db 121 AGAGCCACCTCTCCTCGACGGGCGCAGTCAGAGTGTATTAGACGATCTTAAGCTGTATC	180			
QY 181 CAGCAAAAACCTGCGCAGGCTCCAGGCTCCTCATCTATATGTTGATCCACAGGGCACT	240			
Db 181 CAGCAAAAACCTGCGCAGGCTCCAGGCTCCTCATCTATATGTTGATCCACAGGGCACT	240			
QY 241 GGCATGCGCAGACAGTTTCAGTGGGAGTGGGTCGGGAGACAGCTTCACTCAACATCACT	300			
Db 241 GGCATGCGCAGACAGTTTCAGTGGGAGTGGGTCGGGAGACAGCTTCACTCAACATCACT	300			
QY 301 AGACTGAGGCTGAAAGATTTTTCAGATGATTAATCTGACAGTATGATGATCACTCAG	360			
Db 301 AGACTGAGGCTGAAAGATTTTTCAGATGATTAATCTGACAGTATGATGATCACTCAG	360			
QY 361 ACACCTCAGATCACTTTTCGGCGGAGGAGCCAAAGGTGAGATCAACGAACTGTGGTCA	420			
Db 361 ACACCTCAGATCACTTTTCGGCGGAGGAGCCAAAGGTGAGATCAACGAACTGTGGTCA	420			
QY 421 CCACTCTGTCTTGGCGGCTGGCGGCTTCCGAGAGTGGTGAATCAGGTGAGAGTGGCTCCAG	480			
Db 421 TC-----CGGAGAG	429			
QY 481 GTGACAGTGTGAGTCTGGGGGAGAGCGTGGTCCAGCTGGGAGGTCCCTGAGACTTCC	540			
Db 430 GTGACAGTGTGAGTCTGGGGGAGAGCGTGGTCCAGCTGGGAGGTCCCTGAGACTTCC	489			
QY 541 TGTGACAGCTTGTGATTTCCCTTCAGAAAGCTTTTGCTATGCACTGGGTCGCGCAGGCTCTA	600			
Db 490 TGTGACAGCTTGTGATTTCCCTTCAGAAAGCTTTTGCTATGCACTGGGTCGCGCAGGCTCTA	549			
QY 601 GGCAGAGGGGCTGAGTGGGTGGGAGTATATCATATGATGGAACACTAATAATCAAGCA	660			
Db 550 GGCAGAGGGGCTGAGTGGGTGGGAGTATATCATATGATGGAACACTAATAATCAAGCA	609			
QY 661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAAAGAACACGGTGTATCTA	720			
Db 610 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAAAGAACACGGTGTATCTA	669			
QY 721 AAAATGAACAGCTTGAGAACTGAGAGACAGGCTGTCTATTACTGTGCGAGAGATCAAGNC	780			
Db 670 AAAATGAACAGCTTGAGAACTGAGAGACAGGCTGTCTATTACTGTGCGAGAGATCAAGNC	729			

```
QY 781 CTGTGGGTGACTATGACCACTACTACGTTTGGACGTCTGGGGCAAAAGGACCAAGGTC 840
DB 730 CTGTGGGTGACTATGACCACTACTACGTTTGGACGTCTGGGGCAAAAGGACCAAGGTC 789
QY 841 ACCGTCTCTCAGAGATCCGAACAAAATCTGATCAGGAGAAAGATCTGAACCATCATCCAT 900
DB 790 ACCGTCTCTCAGAGATCCGAACAAAATCTGATCAGGAGAAAGATCTGAACCATCATCCAT 849
QY 901 CACCATTAGTGAAGCTT 918
DB 850 CACCATTAGTGAAGCTT 867

RESULT 10
AD052298
AD052298 standard; DNA; 867 BP.
XX
AC AD052298;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human antibody H11 scFv DNA #2.
XX
KM Antigen binding fragment; H chain V region; L chain V region; C-antigen;
KM neoplasia; cancer; vaccine; gene therapy; human;
KM single chain V region fragment; scFv; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..867
FT FT /*tag= a
FT FT /product= "Human antibody H11 scFv protein"
FT FT /transl_except= (pos:853..864, aa:His-Lys)
FT FT /partial
FT FT /note= "No start and stop codon"
XX
PN US2004091484-A1.
XX
PD 13-MAY-2004.
XX
PF 29-AUG-2003; 2003US-00651453.
XX
PR 22-MAY-1996; 96US-00657449.
PR 22-MAY-1997; 97US-00862124.
PR 13-FEB-2001; 2001US-00782397.
XX
PA (DANM/) DAN M D.
PA (MAIT/) MAITI P K.
PA (KAPL/) KAPLAN H A.
PA (GRAD/) GRAD C.
XX
PI Dan MD, Maitei PK, Kaplan HA, Grad C;
XX
DR WPI: 2004-399136/37.
DR P-PSDB; AD052298.
XX
PT Composition useful for treating neoplasia in patient, comprises antigen
PT binding fragment of antibody specifically recognizing C-antigen
PT recognized by antibody comprising H chain V region and L chain V region.
XX
XX Example 7; SEQ ID NO 16; 56bp; English.
XX
CC The invention relates to a composition comprising an antigen binding
CC fragment of an antibody comprising H chain V region and L chain V region
CC that specifically recognizes C-antigen. The invention is useful for
CC treating a patient with a neoplasia. The antigen binding fragment of the
CC antibody is used as diagnostic and imaging reagents. The invention is
CC useful for genetically altering cells in vivo, to treat various types of
CC cancer. It is also useful in vaccine and gene therapy. The present
CC sequence is human antibody H11 single chain V region fragment (scFv) DNA.
XX
```

```
SQL Sequence 867 BP; 209 A; 229 C; 241 G; 188 T; 0 U; 0 Other:
Query Match 87.1%; Score 799.6; DB 12; Length 867;
Best Local Similarity 94.0%; Pred. No. 7.9e-197;
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

QY 1 GAATTCATGAAAAAACCCTATCCGATCCGAGTTGCACTGGCGTTTGGCTACCGTT 60
DB 1 GAATTCATGAAAAAACCCTATCCGATCCGAGTTGCACTGGCGTTTGGCTACCGTT 60
QY 61 GCGCAGGCGCATATTGTGTGAAGCAAGTCCAGGCAACCTCTTGTCTCCAGGGGAA 120
DB 61 GCGCAGGCGCATATTGTGTGAAGCAAGTCCAGGCAACCTCTTGTCTCCAGGGGAA 120
QY 121 AGAGCCACCTCTCTCTGCAAGGCGCAGTCAAGATGTTAAGTCACTTAACCTGGTAC 180
DB 121 AGAGCCACCTCTCTCTGCAAGGCGCAGTCAAGATGTTAAGTCACTTAACCTGGTAC 180
QY 181 CAGCAGAAACCTGGGCGCAGGCTCCAGGCTCCATCTAATGTCATCCACAGGCGCACT 240
DB 181 CAGCAGAAACCTGGGCGCAGGCTCCAGGCTCCATCTAATGTCATCCACAGGCGCACT 240
QY 241 GGCATGCCAGACAGGTTCAAGTGCAGTGGGTCCGGGACAGACTTCATCTCCATCACT 300
DB 241 GGCATGCCAGACAGGTTCAAGTGCAGTGGGTCCGGGACAGACTTCATCTCCATCACT 300
QY 301 AAGCTGAGACCTGAAGATTTTGCAGTGTATTCTGTCAAGCAATTATGTTAGTCACTCAG 360
DB 301 AAGCTGAGACCTGAAGATTTTGCAGTGTATTCTGTCAAGCAATTATGTTAGTCACTCAG 360
QY 361 AACCTCGATACATTTTGGGCGGAGGAGCAAGTGAAGATCAAGCAAGTGGCTGCA 420
DB 361 AACCTCGATACATTTTGGGCGGAGGAGCAAGTGAAGATCAAGCAAGTGGCTGCA 420
QY 421 CCATCTGTCTTGGCGGTGGCGGTTCCGAGGTGGATGATCAGTGAAGTGGCTCCAG 480
DB 421 TC-----CGAGCAG 429
QY 481 GTTCAGCTGTGTGATCTGGGGGAGGCGGTGTCAGCTCCAGGAGTCCCTGAGATCTCC 540
DB 481 GTTCAGCTGTGTGATCTGGGGGAGGCGGTGTCAGCTCCAGGAGTCCCTGAGATCTCC 540
QY 490 GTTCAGCTGTGTGATCTGGGGGAGGCGGTGTCAGCTCCAGGAGTCCCTGAGATCTCC 489
DB 490 GTTCAGCTGTGTGATCTGGGGGAGGCGGTGTCAGCTCCAGGAGTCCCTGAGATCTCC 489
QY 541 TGTGAGGCTCTGAGATCCCTTTCAGAACTTTGCTATGCACTGGGTCGCGAGGCTCTA 600
DB 541 TGTGAGGCTCTGAGATCCCTTTCAGAACTTTGCTATGCACTGGGTCGCGAGGCTCTA 600
QY 490 TGTGAGGCTCTGAGATCCCTTTCAGAACTTTGCTATGCACTGGGTCGCGAGGCTCTA 549
DB 490 TGTGAGGCTCTGAGATCCCTTTCAGAACTTTGCTATGCACTGGGTCGCGAGGCTCTA 549
QY 601 GGCAGAGGCGTGGAGTGGGTGGCACTTATCATATGATGAAGCACTAATATATACGCA 660
DB 601 GGCAGAGGCGTGGAGTGGGTGGCACTTATCATATGATGAAGCACTAATATATACGCA 660
QY 550 GGCAGAGGCGTGGAGTGGGTGGCACTTATCATATGATGAAGCACTAATATATACGCA 609
DB 550 GGCAGAGGCGTGGAGTGGGTGGCACTTATCATATGATGAAGCACTAATATATACGCA 609
QY 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACATTCAGAGACCGGTGTATCTTA 720
DB 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACATTCAGAGACCGGTGTATCTTA 720
QY 610 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACATTCAGAGACCGGTGTATCTTA 669
DB 610 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACATTCAGAGACCGGTGTATCTTA 669
QY 721 AAAATGAACAGCCTGAGAACTGAGACAGCGGCTGTCTATTAATGTGCGAGAGATCAGAGC 780
DB 721 AAAATGAACAGCCTGAGAACTGAGACAGCGGCTGTCTATTAATGTGCGAGAGATCAGAGC 780
QY 670 AAAATGAACAGCCTGAGAACTGAGACAGCGGCTGTCTATTAATGTGCGAGAGATCAGAGC 729
DB 670 AAAATGAACAGCCTGAGAACTGAGACAGCGGCTGTCTATTAATGTGCGAGAGATCAGAGC 729
QY 781 CTGTGGGTGACTATGACCACTACTACGTTTGGACGTCTGGGGCAAAAGGACCAAGGTC 840
DB 730 CTGTGGGTGACTATGACCACTACTACGTTTGGACGTCTGGGGCAAAAGGACCAAGGTC 789
QY 841 ACCGTCTCTCAGAGATCCGAACAAAATCTGATCAGGAGAAAGATCTGAACCATCATCCAT 900
DB 790 ACCGTCTCTCAGAGATCCGAACAAAATCTGATCAGGAGAAAGATCTGAACCATCATCCAT 849
QY 901 CACCATTAGTGAAGCTT 918
DB 850 CACCATTAGTGAAGCTT 867

RESULT 11
AAD04540/c
```

```

ID      AAD04540 standard; DNA; 867 BP.
XX
AC      AAD04540;
XX
DT      04-JUL-2001 (first entry)
XX
DE      Human H11-single chain variable region (scFv) complementary DNA #2.
XX
KW      Human; monoclonal antibody; Mab; H11; single chain variable region; scFv;
KW      neoplastic disease; melanoma; immunoglobulin IgM; gene therapy; lymphoma;
KW      carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;
KW      neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;
KW      C-antigen; chronic leukaemia; glioma; ds.
XX
OS      Homo sapiens.
XX
PN      US6207153-B1.
XX
PD      27-MAR-2001.
XX
PF      22-MAY-1997; 97US-00862124.
XX
PR      22-MAY-1996; 96US-00657449.
XX
PA      (VIVE-) VIVENTIA BIOTECH INC.
XX
PI      Dan MD, Malti PK, Kaplan HA;
XX
DR      WPI; 2001-289584/30.
XX
PT      Composition comprising antigen binding fragments of an antibody that
PT      recognizes an antigen on neoplastic cells but not on normal cells for use
PT      in diagnosis, imaging and treatment of carcinomas.
XX
XX
XX      Example 7; Col 71-72; 56pp; English.
XX
PS      The present sequence is human monoclonal antibody (Mab), H11-single chain
CC      variable region (scFv) complementary DNA. The invention relates to human
CC      monoclonal antibody (Mab) H11, H11-(scFv) single chain variable (V)
CC      region fragment and their corresponding DNA molecules. H11 antibody is an
CC      immunoglobulin of IgM subclass which is specific to C-antigen found
CC      specifically on neoplastic cells and not on normal cells. H11 is an
CC      antibody obtained from the fusion of peripheral blood lymphocytes of a 64
CC      year old male with a low grade glioma and fused to a human myeloma cell
CC      line to produce a hybridoma designated NBGM1/H11. A pharmaceutical
CC      composition comprising H11 and its derivatives are useful in the
CC      diagnosis, imaging and treatment of neoplastic disease, particularly,
CC      carcinoma, breast carcinoma, lung carcinoma, ovarian carcinoma, colon
CC      carcinoma, gastric carcinoma, prostate carcinoma, lymphoma carcinoma,
CC      neuroblastoma, glioma, soft tissue sarcoma, small cell lung carcinoma,
CC      prostatic adenocarcinoma, B and T cell lymphomas and chronic leukaemia.
CC      H11 DNA is also used in vaccines and gene therapy
XX
SQ      Sequence 867 BP; 189 A; 241 C; 229 G; 208 T; 0 U; 0 Other;
XX
Query Match      86.9%; Score 798; DB 4; Length 867;
Best Local Similarity 93.9%; Pred. No. 2e-196;
Matches 862; Conservative 0; Mismatches 5; Indels 51; Gaps 1;

```

```

DB      687 CAGCAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACGAGGCACT 628
QY      241 GGCATGCCAGACAGGTTCAAGTGGCACTGGGTCGGGACAGACTTCACTTCACCATCAGT 300
DB      627 GGCATGCCAGACAGGTTCAAGTGGCACTGGGTCGGGACAGACTTCACTTCACCATCAGT 568
QY      301 AGACTGGAGCCCTGGAAGATTTTTCAGTGTATTAATCTGTCACAGATAGTGTAGCTCACTCAG 360
DB      567 AGACTGGAGCCCTGGAAGATTTTTCAGTGTATTAATCTGTCACAGATAGTGTAGCTCACTCAG 508
QY      361 ACACCTCAGATCACTTTCGCGGAGGACCAAGGTGAGATCAAAAGAACTGTGGCTGCA 420
DB      507 ACACCTCAGATCACTTTCGCGGAGGACCAAGGTGAGATCAAAAGAACTGTGGCTGCA 448
QY      421 CCATCTGTCTTGGCGGTGGCGGTTCCGAGGTGTGATCAAGTGGAGTGGCTCCAG 480
DB      447 TC-----CGAGCAG 439
QY      481 GTGCAGCTGTGAGAGTCTGGGGAGGCGTGTCCAGCTGGAGAGTCCCTGAGACTCTCC 540
DB      438 GTGCAGCTGTGAGAGTCTGGGGAGGCGTGTCCAGCTGGAGAGTCCCTGAGACTCTCC 379
QY      541 TGTGCAGCTGTGAGATTTCCCTTCAGAACTTTGCTATGCACTGGGTCCGCGAGGCTCA 600
DB      378 TGTGCAGCTGTGAGATTTCCCTTCAGAACTTTGCTATGCACTGGGTCCGCGAGGCTCA 319
QY      601 GGCAGAGGCTGTGAGTGGGTGGCACTTATATATATATATATATATATATATATATATATAT 660
DB      318 GGCAGAGGCTGTGAGTGGGTGGCACTTATATATATATATATATATATATATATATATATAT 259
QY      661 GACTCCGTGAAGGCGGATTCACCATCTTCCAGAGACACTTCCAGAAACCGGTATCTTA 720
DB      258 GACTCCGTGAAGGCGGATTCACCATCTTCCAGAGACACTTCCAGAAACCGGTATCTTA 199
QY      721 AAAATGAACAGCTGTGAGACCTAGAGCAAGCGCTGTATTAATCTGTCGAGAGATCTAGAG 780
DB      198 AAAATGAACAGCTGTGAGACCTAGAGCAAGCGCTGTATTAATCTGTCGAGAGATCTAGAG 139
QY      781 CTGTGGGTGATATGACCACTAAGTGTGGAGTGTGGGCAAGAGGACCAAGGTC 840
DB      138 CTGTGGGTGATATGACCACTAAGTGTGGAGTGTGGGCAAGAGGACCAAGGTC 79
QY      841 ACCGCTCTCTCGAGATCCGAACAAAACCTGATCAGGAAAGATCTGAACCATCACT 900
DB      78 ACCGCTCTCTCGAGATCCGAACAAAACCTGATCAGGAAAGATCTGAACCATCACT 19
QY      901 CACCATTTAGTGAAGCTT 918
DB      18 CACCATTTAGTGAAGCTT 1

```

RESULT 12  
AD052300/C  
ID AD052300 standard; DNA; 867 BP.  
XX  
AC AD052300;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human antibody H11 scFv complementary DNA #2.  
XX  
KW Antigen binding fragment; H chain V region; L chain V region; C-antigen;  
KW neoplasia; cancer; vaccine; gene therapy; human;  
KW single chain V region fragment; scFv; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN US2004091484-A1.  
XX  
PD 13-MAY-2004.  
XX  
PF 29-AUG-2003; 2003US-00651453.

PR 22-MAY-1996; 96US-00657449.  
 PR 22-MAY-1997; 97US-00862124.  
 PR 13-FEB-2001; 2001US-00782397.  
 PA (DANM/) DAN M. D.  
 PA (MATT/) MATTI P. K.  
 PA (KAPL/) KAPLAN H. A.  
 PA (GRAD/) GRAD C.  
 PI Dan MD, Matti PK, Kaplan HA, Grad C;  
 DR WPI, 2004-399136/37.  
 XX  
 XX  
 PT Composition useful for treating neoplasia in patient, comprises antigen  
 PT binding fragment of antibody specifically recognizing C-antigen  
 PT recognized by antibody comprising H chain V region and L chain V region.  
 PS Example 18; SEQ ID NO 18; 56pp; English.  
 XX  
 XX The invention relates to a composition comprising an antigen binding  
 CC fragment of an antibody comprising H chain V region and L chain V region  
 CC that specifically recognizes C-antigen. The invention is useful for  
 CC treating a patient with a neoplasia. The antigen binding fragment of the  
 CC antibody is used as diagnostic and imaging reagents. The invention is of  
 CC useful for genetically altering cells in vivo, to treat various types of  
 CC cancer. It is also useful in vaccine and gene therapy. The present  
 CC sequence is human antibody H11 single chain V region fragment (scfv)  
 CC complementary DNA.  
 XX  
 SO Sequence 867 BP; 189 A; 241 C; 229 G; 208 T; 0 U; 0 Other;  
 Query Match 86.9%; Score 798; DB 12; Length 867;  
 Best Local Similarity 93.9%; Pred. No. 2e-196;  
 Matches 862; Conservative 0; Mismatches 5; Indels 51; Gaps 1;

QY 1 GAATTGATGAAAAAACCCTATCGAGTGCAGTTGCACTGGTGGTTTGGTACCGTT 60  
 DB 867 GAATTGATGAAAAAACCCTATCGAGTGCAGTTGCACTGGTGGTTTGGTACCGTT 808  
 QY 61 GCGCAGGCCGATATTTGTTGACGAGCTTCAGAGCAGCTCTTGTCTCCAGGGGAA 120  
 DB 807 GCGCAGGCCGATATTTGTTGACGAGCTTCAGAGCAGCTCTTGTCTCCAGGGGAA 748  
 QY 121 AGAGCCACCTCTCTCGACAGGCGCAGTCAAGTGTATGTAAGCACTTACCTGGTAC 180  
 DB 747 AGAGCCACCTCTCTCGACAGGCGCAGTCAAGTGTATGTAAGCACTTACCTGGTAC 688  
 QY 181 CACGAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGATGATCCACAGGGCCACT 240  
 DB 687 CACGAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGATGATCCACAGGGCCACT 628  
 QY 241 GGCATGCGACAGAGTTCACTGAGTGGATGCGGAGCAGACTTCACTTCAACATCAGT 300  
 DB 627 GGCATGCGACAGAGTTCACTGAGTGGATGCGGAGCAGACTTCACTTCAACATCAGT 568  
 QY 301 AGACTGAGCCTGAAGATTTTTCAGTGTATTTCTCTCAAGCACTATGTTAGTCACTCAG 360  
 DB 567 AGACTGAGCCTGAAGATTTTTCAGTGTATTTCTCTCAAGCACTATGTTAGTCACTCAG 508  
 QY 361 AACCTCTAGATCACTTTCCGCGGAGGAGCAAGGTGAGATCAACAGCACTGTGGTCA 420  
 DB 507 AACCTCTAGATCACTTTCCGCGGAGGAGCAAGGTGAGATCAACAGCACTGTGGTCA 448  
 QY 421 CCAATCTCTCTGCGGAGTGGCGGTTCCGAGGTGGATCAAGTGAAGGTGGCTCCAG 480  
 DB 447 TC-----CGAGCAG 439  
 QY 481 GTGCACTGTGTGAGTCTGGGGAGGGCTGTCTCAGCTGGAGAGTCCCTGAAGCTTCC 540  
 DB 438 GTGCACTGTGTGAGTCTGGGGAGGGCTGTCTCAGCTGGAGAGTCCCTGAAGCTTCC 379  
 QY 541 TGTGCACTGTGTGAGTCCCTTCAAGAGCTTGTCTATGCACTGGGTCCGCAAGCTCTA 600  
 DB TGTGCACTGTGTGAGTCCCTTCAAGAGCTTGTCTATGCACTGGGTCCGCAAGCTCTA 319

DB 378 TGTGCACTGTGTGAGTCCCTTCAAGAGCTTGTCTATGCACTGGGTCCGCAAGCTCTA 319  
 QY 601 GCGAAGGGGCTGTGAGTGGTGGCACTTATATATGATGAAAGCACTTAAATACAGCA 660  
 DB 318 GCGAAGGGGCTGTGAGTGGTGGCACTTATATATGATGAAAGCACTTAAATACAGCA 259  
 QY 661 GACTCCGTAAGAGGGCGGATTCAGATTCACAGAGACACTTCCAAAGAACGGTGTATCTA 720  
 DB 258 GACTCCGTAAGAGGGCGGATTCAGATTCACAGAGACACTTCCAAAGAACGGTGTATCTA 199  
 QY 721 AAAATGAACGCTGAGAACTGAGGACAGCGCTGTCTATTACTGTGCGAGATCAGAC 780  
 DB 198 AAAATGAACGCTGAGAACTGAGGACAGCGCTGTCTATTACTGTGCGAGATCAGAC 139  
 QY 781 CTGTTGGGTGATATGACCACTTACGTTTGGACGTCGTGGGGCAAGAGGACACGCTC 840  
 DB 138 CTGTTGGGTGATATGACCACTTACGTTTGGACGTCGTGGGGCAAGAGGACACGCTC 79  
 QY 841 ACCGTCCTCAGAGATCCGACAAAACCTGATCAGGAGAAAGANTCTGAACCATCACT 900  
 DB 78 ACCGTCCTCAGAGATCCGACAAAACCTGATCAGGAGAAAGANTCTGAACCATCACT 19  
 QY 901 CACCATTTAGTGAAGCTT 918  
 DB 18 CACCATTTAGTGAAGCTT 1

RESULT 13  
 ADF83553  
 ID ADF83553 standard; DNA; 1103 BP.  
 XX  
 AC ADF83553;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 XX Anti-tetanus toxoid scfv coding sequence.  
 DE Bacteriophage T7; phage display; Fab; antibody; tetanus toxoid; gene; ss.  
 KM  
 XX Chimeric.  
 OS Mammalia.  
 OS Escherichia coli.  
 XX  
 FH Key Location/Qualifiers  
 FT promoter 30..209  
 FT /\*tag= a  
 FT /note= "Lac promoter"  
 FT RBS 196..199  
 FT /\*tag= b  
 FT CDS 210..1103  
 FT /\*tag= d  
 FT sig\_peptide 210..275  
 FT /\*tag= c  
 FT /\*note= "OmpA leader"  
 FT mat\_peptide 276..1100  
 FT /\*tag= e  
 FT /product= "Anti-tetanus toxoid scfv"  
 FT  
 XX WO2003097796-A2.  
 XX  
 XX 27-NOV-2003.  
 PD  
 XX 13-MAY-2003; 2003WO-US014964.  
 PF  
 XX 14-MAY-2002; 2002US-0380318P.  
 PR  
 XX (ALEX-) ALEXION PHARM INC.  
 PA (ROTH/) ROTHER R. P.  
 PA (GEIS/) GEIS D R.  
 XX  
 PI Rother RP, Geis DR;  
 XX  
 DR WPI, 2004-022857/02.

XX New T7 bacteriophage having a Fab fragment, useful for producing and  
 PT screening complex libraries of proteins that bind to particular targets,  
 PT mapping epitopes of antibodies, generating immunogens and isolating  
 PT antibodies.

XX Example 1; Fig 6a-6b; 28pp; English.

XX The present sequence is that of an anti-tetanus toxoid scFv coding  
 CC sequence. It comprises a lac promoter, an OmpA leader sequence, and  
 CC sequence encoding single chain anti-tetanus toxoid VI and VII, followed  
 CC by a His6 tag and haemagglutinin tag. The gene was used in examples from  
 CC the invention describing the construction or Fab expression constructs.  
 CC The invention relates to the T7 bacteriophage display of Fab fragments.  
 CC Host cells and methods of making the phage are described. A claimed  
 CC process for producing a Fab T7 phage display vector comprises: providing,  
 CC in the genome of a T7 phage, a first nucleic acid construct containing  
 CC nucleic acids encoding a light chain fused to a T7 capsid protein  
 CC (preferably 10a or 10b) under regulatory control of a first promoter;  
 CC providing, in the genome of the T7 phage, a second nucleic acid construct  
 CC containing nucleic acids encoding a heavy chain fd under the control of a  
 CC second promoter, which may be the same or different from the first  
 CC promoter.

XX Sequence 1103 BP; 243 A; 303 C; 322 G; 235 T; 0 U; 0 Other;

XX Query Match 49.8%; Score 457; DB 12; Length 1103;  
 XX Best Local Similarity 74.3%; Pred. No. 4.3e-108;  
 XX Matches 628; Conservative 0; Mismatches 190; Indels 27; Gaps 3;

QY 7 ATGAAAAAACCGCTATCGGATCGAGTTCAGCTGCTGCTTCCCTACCGCTGGCGAG 66  
 DB 210 ATGAAAAAACCGCTATCGGATCGAGTTCAGCTGCTGCTTCCCTACCGCTGGCGAG 269  
 QY 67 GCCGATATGTGTGACGAGTCTCCAGGCAACCTCTCTTGTCTCCAGGGAAAGAGCC 126  
 DB 270 GCGG---CCGAGTCAACGAGTCTCCAGGCAACCTCTCTTGTCTCCAGGGAAAGAGCC 326  
 QY 127 ACCCTCTCTGAGGGCCAGTCAAGTGTATGAGCAGTCTTACCTTACCTGTAACAGAG 186  
 DB 327 ACCCTCTCTGAGGGCCAGTCAAGTGTATGAGCAGTCTTACCTTACCTGTAACAGAG 386  
 QY 187 AAACCTGGCAGGCTCCCGAGGCTCCCTCATCTATGTGATCCACGAGGCGCACTGGCAG 246  
 DB 387 AAACCTGGCAGGCTCCCGAGGCTCCCTCATCTATGTGATCCACGAGGCGCACTGGCAG 446  
 QY 247 CCAGACAGGTTAGTGGAGTGGGATCCGGGACAGACTTCACTCTGACATCAGTAGACTG 306  
 DB 447 CCAGACAGGTTAGTGGAGTGGGATCCGGGACAGACTTCACTCTGACATCAGTAGACTG 506  
 QY 307 GAGCCTGAAGATTTTGCAGTGTATTACTGTACAGCACTATGTAGCTCACCTCAGACACT 366  
 DB 507 GAGCCTGAAGATTTTGCAGTGTATTACTGTACAGCACTATGTAGCTCACCTCAGACACT 560  
 QY 367 CAGATCACTTTGGCGGAGGACCAAGGTGAGATCAAAAGCACTGTGGCTGCACCATCT 426  
 DB 561 -----TTGGGCGCAAGGACCAAGGTGAGATCAAAAGCACTGTGGCTGCACCATCT 611  
 QY 427 GTCTGAGGAGTGGGCGGTTCCGAGAGTGTGATCGAGTGGAGTGGCTCCAGAGTGCAG 486  
 DB 612 GGTCTGGGCGGTT-----GGTGGGAGTGTCTCTTAGATCTTCCAGAGTGCAGCTG 662  
 QY 487 CTGTGAGATCTGGGAGGAGCGTGTCCAGCTGGAGAGTCCCTGAGACTCTCTGTGCA 546  
 DB 663 CTGTGAGATCTGGGAGGAGCGTGTCCAGCTGGAGAGTCCCTGAGACTCTCTGTGCA 722  
 QY 547 GCTCTGAGATCCCTCTCAAGACTTGTCTATGCACTGGGTCCGCGAGGCTCTAGGCAAG 606  
 DB 723 GCTTCTGGAGGCACTTCAACATTTATGTGCATCAGCTGGGTGGAGAGGCCCTCTGACAA 782  
 QY 607 GGGCTGAGATGGGTGCGAGTTATATCATATGATGAAAGCACTAAATACGAGACTCC 666  
 DB 783 GGGCTTGAATGGATGGAGGAGATCTTCCCTTCCGTAATACGAAAGTACGACAAACAC 842

QY 667 GTGAAGGGCCGATTCACATCTCCAGAGACACTTCCAGAGACGCGTGTATCTAAATG 726  
 DB 843 TTCAGGGGCAAGTCCCATTCACCGCGAGAAATTCACGAGGCAACCTTACGAGACTG 902  
 QY 727 AACAGCCTGAGAACTGAGAGACAGCGCTGTCTATTACTGTGCGAGATGAGCCGTGG 786  
 DB 903 AGCAGCTGAGATCTGAGAGACAGCGCATATATTATTTGCGAGAGGATACGATTTT 962  
 QY 787 GGTACTATGACCACTACTACGCTTTGACGCTCTGGGCGAAAGGACCAAGTCCGTC 846  
 DB 963 GAGTGACCATGAGATACGCTATGACGCTCTGGGCGAAAGGACCAAGTCCGTC 1022  
 QY 847 TCCTC 851  
 DB 1023 TCAC 1027

RESULT 14  
 AA250588  
 ID AA250588 standard; DNA; 1630 BP.  
 AC AA250588;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 XX HD70scFv-Ck-interleukin 2 encoding DNA.  
 DE  
 XX HD70; single-chain variable fragment; scFv; 17-1A antigen; human; BpCAM;  
 KW epithelial cell adhesion molecule; inflammatory cytokine; IL-2;  
 KW interleukin-2; Ck-domain; kappa light chain constant domain;  
 KW heteroantibody; multifunctional compound; immunoglobulin; cytostatic;  
 KW immunostimulatory; antileukemia; diagnosis; prevention;  
 KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;  
 KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH CDS 39..1613  
 FT /\*tag= a  
 FT /\*product= "HD70scFv-Ck-IL-2 chain"  
 FT /\*tag= b  
 FT /\*label= HD70\_scFv  
 XX  
 PN MO200006605-A2.  
 XX  
 PD 10-FEB-2000.  
 XX  
 XX 28-JUL-1999; 99WO-BP005416.  
 PF  
 XX  
 PR 28-JUL-1998; 98EP-00114082.  
 XX  
 PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.  
 XX  
 PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;  
 XX  
 DR MPI; 2000-195265/17.  
 DR P-PsDB; AA44995.  
 XX  
 PT New multifunctional compounds useful for preventing and/or treating  
 PT malignant cell growth and for detection and diagnosis.  
 XX  
 PS Claim 8; Fig 55B; 166pp; English.  
 XX  
 CC The patent discloses heteroantibodies which are multifunctional compounds  
 CC producible in a mammalian host cell as a secretable and fully functional  
 CC heterodimer of two polypeptide chains, where one of the polypeptide  
 CC chains comprises a CH1-domain (constant domain of an immunoglobulin  
 CC heavy chain) and the other chain comprises CL-domain (constant domain of  
 CC an immunoglobulin light chain). The polypeptide chains further comprise,  
 CC fused to the constant domains at least two (poly)peptides having



CC different receptor or ligand functions, where further at least two of the  
 CC different (poly)peptides lack an intrinsic affinity for one another and  
 CC are linked via the constant domains. The heteromimibodies have  
 CC cytostatic, immunostimulatory, antileukemia and antiproliferative  
 CC activities. These compounds can be used for diagnosing, preventing and  
 CC treating malignant cell growth related to malignancies of haematopoietic  
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,  
 CC melanomas and sarcomas. The present sequence is a DNA encoding right  
 CC chain of a heteromimibody comprising HD70 single-chain Fv (scFv) fragment  
 CC N-terminally linked to human Ck domain (constant domain of immunoglobulin  
 CC -kappa light chain) which bears at its C-terminus the human inflammatory  
 CC cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the  
 CC human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen

XX Sequence 1630 BP; 445 A; 410 C; 408 G; 367 T; 0 U; 0 Other;

SQ Query Match 48.5%; Score 445; DB 3; Length 1630;

Best Local Similarity 76.3%; Pred. No. 6,1e-105; Matches 620; Conservative 0; Mismatches 145; Indels 48; Gaps 4;

52 GCTACCGTTCGCGAGCCGATATGTGTGACGCACTTCACAGGACCCCTGCTTTGCT 111  
 78 GCTACAGGTGTACACTCCAGAGCTCCAGATGACCCAGCTTCACCTCCCTGCTGCATCT 137  
 112 CCAGGGGAAAAGCCACCCCTCTCTCCAGAGGCCAGTCCAGAGTGTAGTAGAGCTACTTA 171  
 138 GTAGGAGACAGAGTCCACATCACTTGCAGGCAAGTCAAG--CATTAGCAGCTATTTA 194  
 172 GCCTGTGACAGAGAAACCTGCGCAGGCTCCAGGCTCCTCATCTANTAGTGATCACC 231  
 195 AATGTGTATCAGAGAAACAGAGACAGCTCCTTAAGCTGTCTATTACTGGGATCTACC 254  
 232 AGGGCCACTGGCATGCGCAAGAGTTCAGTGCAGTGGGTCCGGACAGACTTCACTCTC 291  
 255 CCGGAATCCGGGGTCCCTGACCGATTCAGGCGAGTGAATCTGGACAATTAACACTCTC 314  
 292 ACCATAGATGATGAGAGCTGAAAGTTTTCAGTGTATTACGTACAGAGTATGGTAGC 351  
 315 ACCATAGAGAGCTGAGAGCTGAAAGTTTTCATCTACTTTTGTCAACAGTCTGACAGT 374  
 352 TCACCTCAGACCACTCAGATCACTTTCGGCGAGGAGACCAAGGTGAGATCAACAACAT 411  
 375 TTGCC-----GATCACCTTCGCGCAAGGAGACAGATGACATTCAA----- 416  
 412 GTGGCTGACCATCTGTCTCTGCGGGTGGCGTTCGGAGTGTGGATCAGGTGAGGT 471  
 417 -----GGAGGAGGAGATCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 455  
 472 GGCTCCAGAGTGCAGTGTGAGTCTGGGGAGGCGTGTCCAGCTGGGAGGTCCCTG 531  
 456 GGCTCAGAGGTGAGTGTGAGTCTGGGGAGGCGTGTCCAGCTGGGAGGTCCCTG 515  
 532 AGACTCTCTGTGACAGCTCTGAGATTCCTCTCAGAAAGCTTTGCTATGACCTGGTCCG 591  
 516 AGACTCTCTGTGACAGCTCTGAGATTCCTCTCAGAAAGCTTTGCTATGAGTATGAGT 575  
 592 CAGGCTCTAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATATGATGAGAGCACTAA 651  
 576 CAGGCTCTAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATATGAGAGTAAATAA 635  
 652 TACTAGGAGATCCCGTGAAGGGGCCATTCACATCTCCAGAGACACTTCCAGAACAG 711  
 636 TACTAGGAGATCCCGTGAAGGGGCCATTCACATCTCCAGAGACACTTCCAGAACAG 695  
 712 GTGTATCTAAATGAACAGCTGAGATGAGAGACAGGCTCTATTAATTCTGTGAGAGA 771  
 696 CTGTATCTGCAATGAACAGCTGAGATGAGAGACAGGCTCTATTAATTCTGTGAGAGA 755  
 772 GATCAGAGCTGTGGTGACT-----ATGACCACTACTAGGGTTTGAAGTCTGGGCG 825  
 756 GATATGGGGTGGGAGTGGCTGAGAGACCTTACTACTAGATGATGAGAGTCTGGGCG 815  
 826 AAAGGAGACCAAGGTCAACCTGTCTCTCAAGATCC 858

DB 816 CAAGGACCAAGGTCAACCTGTCTCTCAAGATCC 848

RESULT 15  
 AA250587

ID AA250587 strand; DNA; 1630 BP.

AA250587;

23-MAY-2000 (first entry)

DE HD70scFv-CH1-GM-CSF chain encoding DNA.

XX HD70, single-chain variable fragment; scFv; 17-1A antigen; human; EPCAM;  
 KW epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;  
 KW granulocyte/macrophage colony stimulating factor; heteromimibody;  
 KW CH1-domain; multifunctional compound; heavy chain constant domain;  
 KW immunoglobulin; cytostatic; immunostimulatory; antileukemia; diagnosis;  
 KW antiproliferative; prevention; treatment; malignant; haematopoietic cell;  
 KW lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 39..1610

XX FT /tag= a

XX FT /product= "HD70scFv-CH1-GM-CSF chain"

XX FT misc\_feature

XX FT 96..842

XX FT /\*tag= b

XX FT /label= HD70\_scFv

XX PN WO200006605-A2.

XX PD 10-FEB-2000.

XX PF 28-JUL-1999; 99WO-EP005416.

XX PR 28-JUL-1998; 98EP-00114082.

XX PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.

XX PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zetcl F;

XX DR WPI; 2000-195265/17.

XX DR P-PSDB; AAY44994.

XX PT New multifunctional compounds useful for preventing and/or treating

XX PT malignant cell growth and for detection and diagnosis.

XX PS Claim 8; Fig 55A; 166pp; English.

XX CC The patent discloses heteromimibodies which are multifunctional compounds

XX CC producible in a mammalian host cell as a secretable and fully functional

XX CC heterodimer of two polypeptide chains, where one of the polypeptide

XX CC chains comprises, a CH1-domain (constant domain of an immunoglobulin

XX CC heavy chain) and the other chain comprises C $\gamma$ -domain (constant domain of

XX CC an immunoglobulin light chain). The polypeptide chains further comprise,

XX CC fused to the constant domains at least two (poly)peptides having

XX CC different receptor or ligand functions, where further at least two of the

XX CC different (poly)peptides lack an intrinsic affinity for one another and

XX CC are linked via the constant domains. The heteromimibodies have

XX CC cytostatic, immunostimulatory, antileukemia and antiproliferative

XX CC activities. These compounds can be used for diagnosing, preventing and

XX CC treating malignant cell growth related to malignancies of haematopoietic

XX CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,

XX CC melanomas and sarcomas. The present sequence is a DNA encoding left chain

XX CC of a heteromimibody comprising HD70 single-chain Fv (scFv) fragment N-

XX CC terminally linked to human CH1 domain which bears at its C-terminus the

XX CC human inflammatory cytokine granulocyte/macrophage colony stimulating

XX CC factor (GM-CSF), plus a hexahistidine sequence for ease of purification.

XX CC HD70 scFv specifically recognises the human epithelial cell adhesion

XX CC molecule (EPCAM) also called 17-1A antigen



XX Sequence 1630 BP; 376 A; 484 C; 437 G; 333 T; 0 U; 0 Other;

Query Match 48.5%; Score 445; DB 3; Length 1630;  
Best Local Similarity 76.3%; Pred. No. 6.1e-105;  
Matches 620; Conservative 0; Mismatches 145; Indels 48; Gaps 4;

QY 52 GCTACCGTTGCGAGGCCGATATTTGTTGACGCACTTCACAGGCACTCTTGTCT 111  
DB 78 GCTACAGGTGTATCACTCCAGCTCCAGATGACCAGTCTCCATCTCCCTGCTGCATCT 137  
QY 112 CCAGGGAAAGAGCCACCTCTCTCTGACGGCCAGTCAAGTGTATGACAGTACTTA 171  
DB 138 GTAGGAGACAGACTCACTCACTTCCGGGCAAGTCAAG---CATTAGCACTATTTA 194  
QY 172 GCTGTACAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGTCATCC 231  
DB 195 AATTGGTATCAGCAAAACAGGACAGCTCTTAAGCTGCTCATTTACTGGGATCTACC 254  
QY 232 AGGGCACTGGCATGTCAGACAGTTCAGTGGCAGTGGGTCCGGACAGACTTCACTTC 291  
DB 255 CCGGAATCCGGGCTCCCTGACCATTCAGCGCAGTGAATCTGGGACAAATTACACTTC 314  
QY 292 ACCATCAGTAGACTGAGCCTGAAGATTTTGACGTATTACTGACAGATATGATAGC 351  
DB 315 ACCATCAGACGCTGACGCTGAAGATTTTGCTACTTCTTGTCAACAGTCTGACAGT 374  
QY 352 TCACCTCAGACACCTCAGATCACTTTCGGCGAGGAGCCAGGTGAGATCAACGAGCT 411  
DB 375 TTGCC-----GATCACCTTCGGGCAAGGACACAGACTGACATTCNA----- 416  
QY 412 GTGGCTGCACCATCTGTCTCTGGCGGTGGCGGTTCCGAGGTGTGATCAGGTGAGGT 471  
DB 417 -----GGAGGAGAGGATCAGGTGTGTGTAGCGGCGGCGC 455  
QY 472 GGTCCAGAGTGCAGTGTGAGTCTGGGGGAGGCGGTGTCAGCCTGGGAGGTCCCTG 531  
DB 456 GGTCCAGAGTGCAGTGTGAGTCTGGGGGAGGCGGTGTCAGCCTGGGAGGTCCCTG 515  
QY 532 AGACTCTCTGTGACAGCTCTGGAATCCCTTCAGAGCTTGTCTATGCACTGGTCCGC 591  
DB 516 AGACTCTCTGTGACAGCTCTGGAATCATTCAAGTATGATGCACTGGGTCGC 575  
QY 592 CAGGCTTAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGAAAGCACTAAA 651  
DB 576 CAGGCTCCAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGAAATATAA 635  
QY 652 TACTACGACAGCTCCGTGAAGGGCGGATTCAACCATCTCCAGAGACACTTCCAAAGACAG 711  
DB 636 TACTATGACAGCTCCGTGAAGGGCGGATTCAACCATCTCCAGAGACAAATCCAAAGACAG 695  
QY 712 GTGTATCTTAAAAATGAACAGCTGAGAACTGAGACACAGGCTGTCTATTACTGTGCGAGA 771  
DB 696 CTGTATCTGCAATGAACAGCTGAGAGTGAAGACACGGCTGTGTATTACTGTGCGAAA 755  
QY 772 GATCAGAGCTGTGGGTGACT-----ATGACCACTACTACGGTTTGAACGTCTGGGCG 825  
DB 756 GATATGGGCTGGGCGAGTGGTGGAGACCTTACTACTACGATATGAGCGTCTGGGCGC 815  
QY 826 AAAGGAGACAGGTCACCGTCTCCCTCAGGATCC 858  
DB 816 CAAGGAGACAGGTCACCGTCTCCCTCAGGATCC 848

Search completed: February 18, 2005, 06:09:11  
Job time : 624 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: February 18, 2005, 05:23:45 ; Search time 203 Seconds  
(Without alignments)  
7399.517 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 918  
Sequence: 1 GAATTCATCAAAAAACCCG.....ATCACCATTAATGAAAGCTT 918

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/1/lna/5A\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/lna/5B\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/lna/5A\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/lna/5B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/lna/PTUS\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/lna/backfileseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	3	US-08-862-124-13 Sequence 13, Appl
2	916.4	99.8	918	3	US-08-862-124-15 Sequence 15, Appl
3	799.6	87.1	867	3	US-08-862-124-16 Sequence 16, Appl
4	798	86.9	867	3	US-08-862-124-18 Sequence 18, Appl
5	361	39.3	450	3	US-08-862-124-6 Sequence 6, Appl
6	359.4	39.2	450	3	US-08-862-124-4 Sequence 4, Appl
7	345.2	37.6	783	3	US-08-487-283A-19 Sequence 19, Appl
8	343.6	37.4	1848	1	US-08-447-422-15 Sequence 15, Appl
9	324.4	35.3	543	3	US-08-862-124-1 Sequence 1, Appl
10	324.4	35.3	543	3	US-08-862-124-3 Sequence 3, Appl
11	319.8	34.8	1413	4	US-09-472-087-61 Sequence 61, Appl
12	318.4	34.7	4691	3	US-08-591-632-43 Sequence 43, Appl
13	318.4	34.7	4691	3	US-08-591-632-43 Sequence 43, Appl
14	318.4	34.7	6166	3	US-08-591-632-51 Sequence 51, Appl
15	318.4	34.7	6166	3	US-08-591-632-51 Sequence 51, Appl
16	310.6	33.8	678	4	US-09-456-090A-49 Sequence 49, Appl
17	310.6	33.8	678	4	US-09-456-090A-85 Sequence 85, Appl
18	310.6	33.8	678	4	US-09-453-234-49 Sequence 49, Appl
19	310.6	33.8	678	4	US-09-453-234-85 Sequence 85, Appl
20	305.8	33.3	678	4	US-09-456-090A-37 Sequence 37, Appl
21	305.8	33.3	678	4	US-09-456-090A-41 Sequence 41, Appl
22	305.8	33.3	678	4	US-09-456-090A-71 Sequence 71, Appl
23	305.8	33.3	678	4	US-09-453-234-37 Sequence 37, Appl
24	305.8	33.3	678	4	US-09-453-234-41 Sequence 41, Appl
25	303.6	33.1	1797	1	US-08-442-542-17 Sequence 17, Appl
26	303.6	33.1	1797	1	US-08-442-542-17 Sequence 17, Appl
27	303.6	33.1	1797	3	US-08-765-469-17 Sequence 17, Appl

28	303.4	33.1	369	4	US-09-424-840B-5 Sequence 5, Appl
29	302.6	33.0	678	4	US-09-456-090A-73 Sequence 73, Appl
30	302.6	33.0	678	4	US-09-453-234-73 Sequence 73, Appl
31	301	32.8	678	4	US-09-456-090A-79 Sequence 79, Appl
32	301	32.8	678	4	US-09-453-234-79 Sequence 79, Appl
33	301	32.8	948	4	US-09-859-053-33 Patent No. 5455030
34	300.6	32.7	752	6	5455030-12 Patent No. 5455030
35	300.6	32.7	752	6	5455030-12 Patent No. 5455030
36	300.2	32.7	672	4	US-09-456-090A-51 Sequence 51, Appl
37	300.2	32.7	672	4	US-09-453-234-51 Sequence 51, Appl
38	299.8	32.7	708	4	US-09-472-087-40 Sequence 40, Appl
39	299.8	32.7	708	4	US-09-472-087-56 Sequence 56, Appl
40	299.4	32.6	970	4	US-09-859-053-37 Sequence 37, Appl
41	298.2	32.5	372	4	US-09-424-840B-15 Sequence 15, Appl
42	297	32.4	672	4	US-09-456-090A-39 Sequence 39, Appl
43	297	32.4	672	4	US-09-456-090A-75 Sequence 75, Appl
44	297	32.4	672	4	US-09-453-234-39 Sequence 39, Appl
45	297	32.4	672	4	US-09-453-234-75 Sequence 75, Appl

## ALIGNMENTS

```
RESULT 1
US-08-862-124-13
; Sequence 13, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Malti, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; TITLE OF INVENTION: DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,124
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 918 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..906, 913..918)
; US-08-862-124-13
; Query Match 100.0%; Score 918; DB 3; Length 918;
; Best Local Similarity 100.0%; Pred. No. 1.8e-252;
```

Matches	918;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	GAATTCATGAAAAA	CCGCTATCGCATCGAGTTGCACTGGCTGGTTCCTACCGTT	60					
DB	1	GAATTCATGAAAAA	CCGCTATCGCATCGAGTTGCACTGGCTGGTTCCTACCGTT	60					
QY	61	GGCAGAGCCGATATGTTGA	CGAGTCTCCAGGCAACCTCTGTTCTCCAGGGGAA	120					
DB	61	GGCAGAGCCGATATGTTGA	CGAGTCTCCAGGCAACCTCTGTTCTCCAGGGGAA	120					
QY	121	AAGAGCCACCTCTCCGCA	GGGCGACGTCAAGGTGTAAGACGCACTTAAGCTGGTAC	180					
DB	121	AAGAGCCACCTCTCCGCA	GGGCGACGTCAAGGTGTAAGACGCACTTAAGCTGGTAC	180					
QY	181	CAGCAGAAACCTGGCCAG	GGCTCCAGGCTCTCATCTATGTCATCCAGGGCCACT	240					
DB	181	CAGCAGAAACCTGGCCAG	GGCTCCAGGCTCTCATCTATGTCATCCAGGGCCACT	240					
QY	241	GGCATCCAGACAGGTTCA	GTGAGTGGGTCCGGACAGACTTCACTCTCACCATCAGT	300					
DB	241	GGCATCCAGACAGGTTCA	GTGAGTGGGTCCGGACAGACTTCACTCTCACCATCAGT	300					
QY	301	AGACTGGACCTGAAATTT	GAAGTGTATTACTGTCAAGATGATGATGATCACTCAG	360					
DB	301	AGACTGGACCTGAAATTT	GAAGTGTATTACTGTCAAGATGATGATGATCACTCAG	360					
QY	361	ACACCTCAGATCACTTTC	CGCGAGGAGCAACAGTGGAGTCAAAAGAACTGTGGCTGCA	420					
DB	361	ACACCTCAGATCACTTTC	CGCGAGGAGCAACAGTGGAGTCAAAAGAACTGTGGCTGCA	420					
QY	421	CCATCTGTCTCTGGCGG	GTGGGTTCCGAGGTGTGATCAGGTGAGGTGCTCCAG	480					
DB	421	CCATCTGTCTCTGGCGG	GTGGGTTCCGAGGTGTGATCAGGTGAGGTGCTCCAG	480					
QY	481	GTGCACTGTGAGTCTGG	GGGAGGCGGTGTCAGCTGGGAGGTCCCTGAGACTCTCC	540					
DB	481	GTGCACTGTGAGTCTGG	GGGAGGCGGTGTCAGCTGGGAGGTCCCTGAGACTCTCC	540					
QY	541	TGTGACAGCTTGATTC	CCCTTCAGAAAGCTTGTCTATGCACTGGGTCCGCAAGCTCTA	600					
DB	541	TGTGACAGCTTGATTC	CCCTTCAGAAAGCTTGTCTATGCACTGGGTCCGCAAGCTCTA	600					
QY	601	GGCAGAGGCGTGAAGT	GGGTGCGAGTTATCAATGATGAGCACTAAATCTAGCA	660					
DB	601	GGCAGAGGCGTGAAGT	GGGTGCGAGTTATCAATGATGAGCACTAAATCTAGCA	660					
QY	661	GACTCGGTGAAGGCGG	ATTCACCATCTCCAGAGCACTTCCAAAGAACAGGTGTATCTA	720					
DB	661	GACTCGGTGAAGGCGG	ATTCACCATCTCCAGAGCACTTCCAAAGAACAGGTGTATCTA	720					
QY	721	AAATGAACAGCTGAG	AACTGAGACAGCGCTGTCTATTACTGTGGAAGATCAGAGC	780					
DB	721	AAATGAACAGCTGAG	AACTGAGACAGCGCTGTCTATTACTGTGGAAGATCAGAGC	780					
QY	781	CTGTGGGTGATCTATG	ACCTACTACGTTTGGAGCTCTGGGGCAAAAGGACCAAGCTC	840					
DB	781	CTGTGGGTGATCTATG	ACCTACTACGTTTGGAGCTCTGGGGCAAAAGGACCAAGCTC	840					
QY	841	ACCGTCTCTCAGAGT	CCGAAACAAATCTAGTCAGGAGAAAGATCTGAACCATCAGT	900					
DB	841	ACCGTCTCTCAGAGT	CCGAAACAAATCTAGTCAGGAGAAAGATCTGAACCATCAGT	900					
QY	901	CACCATTAAGTAAAG	CTT 918						
DB	901	CACCATTAAGTAAAG	CTT 918						

RESULT 2  
US-08-862-124-15/c  
; Sequence 15, Application US/08862124  
; Patent No. 6207153  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.

APPLICANT: Maity, Pradip K.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT  
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 918 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-862-124-15  
Query Match 99.8%; Score 916.4; DB 3; Length 918;  
Best Local Similarity 99.9%; Pred. No. 5.1e-252;  
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GAATTCATGAAAAA	CCGCTATCGCATCGAGTTGCACTGGCTGGTTCCTACCGTT	60
DB	918	GAATTCATGAAAAA	CCGCTATCGCATCGAGTTGCACTGGCTGGTTCCTACCGTT	859
QY	61	GGCAGAGCCGATATGTTGA	CGAGTCTCCAGGCAACCTCTGTTCTCCAGGGGAA	120
DB	858	GGCAGAGCCGATATGTTGA	CGAGTCTCCAGGCAACCTCTGTTCTCCAGGGGAA	799
QY	121	AAGAGCCACCTCTCCGCA	GGGCGACGTCAAGGTGTAAGACGCACTTAAGCTGGTAC	180
DB	798	AAGAGCCACCTCTCCGCA	GGGCGACGTCAAGGTGTAAGACGCACTTAAGCTGGTAC	739
QY	181	CAGCAGAAACCTGGCCAG	GGCTCCAGGCTCTCATCTATGTCATCCAGGGCCACT	240
DB	738	CAGCAGAAACCTGGCCAG	GGCTCCAGGCTCTCATCTATGTCATCCAGGGCCACT	679
QY	241	GGCATCCAGACAGGTTCA	GTGAGTGGGTCCGGACAGACTTCACTCTCACCATCAGT	300
DB	678	GGCATCCAGACAGGTTCA	GTGAGTGGGTCCGGACAGACTTCACTCTCACCATCAGT	619
QY	301	AGACTGGACCTGAAATTT	GAAGTGTATTACTGTCAAGATGATGATGATCACTCAG	360
DB	618	AGACTGGACCTGAAATTT	GAAGTGTATTACTGTCAAGATGATGATGATCACTCAG	559
QY	361	ACACCTCAGATCACTTTC	CGCGAGGAGCAACAGTGGAGTCAAAAGAACTGTGGCTGCA	420
DB	558	ACACCTCAGATCACTTTC	CGCGAGGAGCAACAGTGGAGTCAAAAGAACTGTGGCTGCA	499
QY	421	CCATCTGTCTCTGGCGG	GTGGGTTCCGAGGTGTGATCAGGTGAGGTGCTCCAG	480

Db 498 CCATCTGTCTTGCGGCTGCGGTTCCGAGGCTGTGATCAAGTGGAGTGGCTCCGAG 439  
Qy 491 GTGCAGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 540  
Db 438 GTGCAGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 379  
Qy 541 TGTGAGGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 600  
Db 378 TGTGAGGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 319  
Qy 601 GCGAAGGCGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 660  
Db 318 GCGAAGGCGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 259  
Qy 661 GACTCCGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 720  
Db 258 GACTCCGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 199  
Qy 721 AAAATGAACAGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 780  
Db 198 AAAATGAACAGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 139  
Qy 781 CTGTTGGGTGACTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 840  
Db 138 CTGTTGGGTGACTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 79  
Qy 841 ACCGTCTCTCAGATTCGGAACAAACTGATCAGCGAAGAGTCTGAACCATGACCAT 900  
Db 78 ACCGTCTCTCAGATTCGGAACAAACTGATCAGCGAAGAGTCTGAACCATGACCAT 19  
Qy 901 CACCATGTGTGAAGCTT 918  
Db 18 CACCATGTGTGAAGCTT 1

## RESULT 3

US-08-862-124-16

Sequence 16, Application US/08862124

Patent No. 6207153

GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

APPLICANT: Maiti, Pradipt K.

APPLICANT: Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT

TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE

TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison &amp; Foerster LLP

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/862,124

FILING DATE: 22-MAY-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Lehnardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 16:

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:  
LENGTH: 867 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1..855, 862..867)  
US-08-862-124-16

Query Match 87.1%; Score 799.6; DB 3; Length 867;  
Best Local Similarity 94.0%; Pred. No. 1.3e-218;  
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

Qy 1 GAATTCATGAAAAAACCCTATTCGCGATCGAGTTGCACTGGCTGTTCCGTAACGTT 60  
Db 1 GAATTCATGAAAAAACCCTATTCGCGATCGAGTTGCACTGGCTGTTCCGTAACGTT 60  
Qy 61 GCGCAGCGCGATATTTGTGTGACGAGTCTCCAGGCAACCTGTTCTTCTCCAGGGGAA 120  
Db 61 GCGCAGCGCGATATTTGTGTGACGAGTCTCCAGGCAACCTGTTCTTCTCCAGGGGAA 120  
Qy 121 AGAGCCACCCTCTCCTGAGGCGCAGTCAAGTGTATGAGGAGCTACTTACCTGGTAC 180  
Db 121 AGAGCCACCCTCTCCTGAGGCGCAGTCAAGTGTATGAGGAGCTACTTACCTGGTAC 180  
Qy 181 CAGCAAAAACCTGCGCAGGCTCCAGGCTCCTCATCTATGTGTCATCCACAGGGCACT 240  
Db 181 CAGCAAAAACCTGCGCAGGCTCCAGGCTCCTCATCTATGTGTCATCCACAGGGCACT 240  
Qy 241 GGCATGCCAGACAGGTTCAATGAGGTCAGTGGTCCGGGACAGACTTCACTTCAACATCA 300  
Db 241 GGCATGCCAGACAGGTTCAATGAGGTCAGTGGTCCGGGACAGACTTCACTTCAACATCA 300  
Qy 301 AGACTGAGCCCTGAAGATTTTGCAGTGTATCTGTCAAGCAGTATGATGCTCACTCAG 360  
Db 301 AGACTGAGCCCTGAAGATTTTGCAGTGTATCTGTCAAGCAGTATGATGCTCACTCAG 360  
Qy 361 ACACCTCAGATCACTTTCCGCGAGGAGCAAGGTGAGATCAAAAGAACTGTGCTGCA 420  
Db 361 ACACCTCAGATCACTTTCCGCGAGGAGCAAGGTGAGATCAAAAGAACTGTGCTGCA 420  
Qy 421 CCATCTGTCTCTGCGGCTGCGGCTCCGAGGTGTGATCAGTGTGAGTGGTCCGAG 480  
Db 421 TC-----CGAGCAG 429  
Qy 481 GTGCAGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 540  
Db 481 GTGCAGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 540  
Qy 541 TGTGAGGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 600  
Db 541 TGTGAGGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 600  
Qy 601 GCGAAGGCGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 660  
Db 601 GCGAAGGCGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 660  
Qy 661 GACTCCGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 720  
Db 661 GACTCCGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 720  
Qy 721 AAAATGAACAGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 780  
Db 721 AAAATGAACAGCTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 780  
Qy 781 CTGTTGGGTGACTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 840  
Db 781 CTGTTGGGTGACTGTGTGAGTCTGGGGGAGGCGGTGTCCAGCTGGGAGTCCCTGAGACTCTCC 840  
Qy 841 ACCGTCTCTCAGATTCGGAACAAACTGATCAGCGAAGAGTCTGAACCATGACCAT 900  
Db 841 ACCGTCTCTCAGATTCGGAACAAACTGATCAGCGAAGAGTCTGAACCATGACCAT 900



APPLICATION NUMBER: US/08/862,124  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Leinhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 450 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-862-124-6

Query Match 39.3%; Score 361; DB 3; Length 450;  
Best Local Similarity 100.0%; Pred. No. 2.7e-93;  
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 GATATTGTGTGACGAGCTCCAGGACCCCTGTCTTGTCTCAGGGGAAAGGCCACC 129  
DB 378 GATATTGTGTGACGAGCTCCAGGACCCCTGTCTTGTCTCAGGGGAAAGGCCACC 319  
QY 130 CTCTCCTGAGGGCCAGTCAAGAGTTAGTACGAGTCTTACCTGTGATCCAGAGAAA 189  
DB 318 CTCTCCTGAGGGCCAGTCAAGAGTTAGTACGAGTCTTACCTGTGATCCAGAGAAA 259  
QY 190 CTTGCGCAGGCTCCAGGCTCTCATCTATGTGTCATCCACAGGGCCACTGGCATGCCA 249  
DB 258 CTTGCGCAGGCTCCAGGCTCTCATCTATGTGTCATCCACAGGGCCACTGGCATGCCA 199  
QY 250 GACAGGTTGAGTGGCAGTGGGTCGGGGAACAAGTCTACTCTACCACTCACTGATGAGCTGGAG 309  
DB 198 GACAGGTTGAGTGGCAGTGGGTCGGGGAACAAGTCTACTCTACCACTCACTGATGAGCTGGAG 139  
QY 310 CCGTAAGATTTTGCAGTGTATTACTGTCAAGAGTATGATGATCACTTCACTGATGAGCTGGAG 369  
DB 138 CCGTAAGATTTTGCAGTGTATTACTGTCAAGAGTATGATGATCACTTCACTGATGAGCTGGAG 79  
QY 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGAACTGTGGCTGCACCATCTGTC 429  
DB 78 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGAACTGTGGCTGCACCATCTGTC 19  
QY 430 T 430  
DB 18 T 18

RESULT 6  
US-08-862-124-4  
Sequence 4, Application US/08862124  
Patent No. 6207153  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
APPLICANT: Maici, Pradip K.  
APPLICANT: Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT  
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
TITLE OF INVENTION: DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/862,124  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Leinhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 450 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..450  
US-08-862-124-4

Query Match 39.2%; Score 359.4; DB 3; Length 450;  
Best Local Similarity 99.7%; Pred. No. 7.8e-93;  
Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 70 GATATTGTGTGACGAGCTCCAGGACCCCTGTCTTGTCTTCCAGGGGAAAGGCCACC 129  
DB 73 GATATTGTGTGACGAGCTCCAGGACCCCTGTCTTGTCTTCCAGGGGAAAGGCCACC 132  
QY 130 CTCTCCTGAGGGCCAGTCAAGAGTTAGTACGAGTCTTACCTGTGATCCAGAGAAA 189  
DB 133 CTCTCCTGAGGGCCAGTCAAGAGTTAGTACGAGTCTTACCTGTGATCCAGAGAAA 192  
QY 190 CTTGCGCAGGCTCCAGGCTCTCATCTATGTGTCATCCACAGGGCCACTGGCATGCCA 249  
DB 193 CTTGCGCAGGCTCCAGGCTCTCATCTATGTGTCATCCACAGGGCCACTGGCATGCCA 252  
QY 250 GACAGGTTGAGTGGCAGTGGGTCGGGGAACAAGTCTACTCTACCACTCACTGATGAGCTGGAG 309  
DB 253 GACAGGTTGAGTGGCAGTGGGTCGGGGAACAAGTCTACTCTACCACTCACTGATGAGCTGGAG 312  
QY 310 CCGTAAGATTTTGCAGTGTATTACTGTCAAGAGTATGATGATCACTTCACTGATGAGCTGGAG 369  
DB 313 CCGTAAGATTTTGCAGTGTATTACTGTCAAGAGTATGATGATCACTTCACTGATGAGCTGGAG 372  
QY 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGAACTGTGGCTGCACCATCTGTC 429  
DB 373 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGAACTGTGGCTGCACCATCTGTC 432  
QY 430 T 430  
DB 433 T 433

RESULT 7  
US-08-487-283A-19  
Sequence 19, Application US/08487283A  
Patent No. 6355245  
GENERAL INFORMATION:  
APPLICANT: Evans, Mark J.  
APPLICANT: Matie, Louis A.  
APPLICANT: Mueller, Eileen Elliott  
APPLICANT: Nye, Steven H.  
APPLICANT: Rollins, Scott  
APPLICANT: Rother, Russell P.  
APPLICANT: Springhorn, Jeremy P.  
APPLICANT: Squinto, Stephen P.

APPLICANT: Thomas, Thomas C.  
APPLICANT: Wilkins, James A.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT  
OF INFLAMMATORY DISEASES  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Seth A. Fidel  
STREET: 25 Science Park (Alexion)  
CITY: New Haven  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06511  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.4mb storage  
COMPUTER: Macintosh Celis 610  
OPERATING SYSTEM: System 7  
SOFTWARE: Wordperfect 3.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,283A  
FILING DATE: June 7, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/236,208  
FILING DATE: 02-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Seth A. Fidel  
REGISTRATION NUMBER: 38,449  
REFERENCE/DOCKET NUMBER: ALX-152.1 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203) 776-1790  
TELEFAX: (203) 772-3655  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 783 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: N19/8 scrv (His Tagged)  
US-08-487-283A-19

Query Match 37.6%; Score 345.2; DB 3; Length 783;  
Best Local Similarity 69.3%; Pred. No. 1.2e-88;  
Matches 552; Conservative 0; Mismatches 193; Indels 51; Gaps 4;

66 GGGCCATATTGTTGTACCGCAGTCTCCAGCACCCCTGTTTGTCTCCAGGGAAAGAC 125  
|||  
3 GGGCAATATTGTGCTGACCCAACTCCAGCTTCTTGGCTGTGCTTGGGCGAGAGGC 62  
|||  
126 CACCTCTCTGCGAGGGCCAGTCAGAGTGTAGTAG-----CAGCTACTTAGCTG 176  
|||  
63 CACCAATCTCTGAGAGCCAGTGAAGTGTGATGATGACAAATAGTTTATGACATG 122  
|||  
177 GTACGAGAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGATGTCACACGAGGC 236  
|||  
123 GTACGAGAGAAACGAGACGACCAAACTCTCATCTTCTTGATCCAACTAGAA 182  
|||  
237 CACTGGCATGCCAGACAGGTTCACTGTCAGTGGTCCGGAGACAGACTTCACTTCA 296  
|||  
183 ATCTGGGATCCCTGCGACAGGTTCACTGTCAGTGGTCTTAGGACGACTTCACTTCA 242  
|||  
297 CAGTAGACTGAGAGCTGAGATTTGACGATGATTACTGACAGATAGGTAGTCACTC 356  
|||  
243 TGATCTGTGAGAGGCTGATGATCTGCAACCTATTACTGTACCA-----AAA 290  
|||  
357 TCAGACACTCAGATCATCTTTCGCGAGAGGACCAAGGTGAGATCAAAAGAACTGTGC 416  
|||  
291 TATATGAGTTCCGAAACAGCTTCGAGAGGGGAGCAAGCTGGAATAAAGGA----- 343  
|||  
417 TGACACATCTGTCTGCGGCGGTGCGGCTTCGAGAGTGTGATCAAGTGTGAGTGGCTC 476  
|||  
344 -----CCGAGAGTGGCGGCTGCGGCTGCGGAGGATCGGAGAGGCTCTGAGACT 389  
|||  
477 CCAGGTGACGTGTGGAAGTCTGGGAGAGGCGTGTCCAGCTCGGAGAGTCTCTGAGACT 536  
|||

DB 390 GAGCTGACAGCTCGTGGAGTCTGGGGAGACCTTATGTAAGCTTGAAGGCTCCCTAACT 449  
|||  
QY 537 CTCTGTGAGCCTTGATTCCTCTTCCAGAACTTTGCTATGCACTGGGTCCGCGAGC 596  
|||  
DB 450 CTCTGTGAGCCTTGATTCCTCTTCCAGAACTTTGCTATGTAAGCTTGGGTTCGCGAGT 509  
|||  
QY 597 TCTAGCAAGGGCTGAGTGGGTGCGGCTTATCATATGATGTAAGACATAATPACTA 656  
|||  
DB 510 TCCAGAGAAAGGCTGAGTGGGTGCGGCTTATCATATGTAAGTATGATGACTTACTA 569  
|||  
QY 657 CGCAGACTCCGTGAGAGGCGGATTCACCATCTCCAGAGACACTTCCAAAGACGATGA 716  
|||  
DB 570 TCCAGACACTGTGAGAGGCGGATTCACCATCTCCAGAGACATGCAAGAGACCTTGA 629  
|||  
QY 717 TCTAAATGAACAGCTGAGACTGAGAGACAGGCTGTCTATCTGTGCGAGAGATCA 776  
|||  
DB 630 TCTGCAATGAGCACTGAGACTGAGAGACAGCCTGTATTTCTGTGTAAGAGA--- 686  
|||  
QY 777 GAGCTGTGGGTGATGACCACTACTACGCTTGAACGCTGGGGCAAGGACAC 836  
|||  
DB 687 -----GACTTATTACTACGGGATTAATGCTCTTCGATGCTGGGCAAGAGAC 740  
|||  
QY 837 GGTACCGCTCTCTCA 852  
|||  
DB 741 GGTACCGCTCTCTCA 756  
|||

RESULT 8  
US-08-447-422-15  
Sequence 15, Application US/08447422  
Patent No. 5686579  
GENERAL INFORMATION:  
APPLICANT: SHAMT, Ezekiel Y.  
APPLICANT: ROTHSTEIN, Aser  
TITLE OF INVENTION: Use of Antibody/Antigen Interactions To  
Protect or Modulate Biological Activity  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/447,422  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: US 08/081,410  
FILING DATE: 22-JUN-1993  
APPLICATION NUMBER: US 07/938,505  
FILING DATE: 31-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/205,748  
FILING DATE: 21-JUN-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17923/102 HYL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELFX: 904136  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1848 base pairs





APPLICANT: Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
TITLE OF INVENTION: DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/862,124  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ. ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 543 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-862-124-3

Query Match 35.3%; Score 324.4; DB 3; Length 543;  
Best Local Similarity 89.3%; Pred. No. 8.7e-83;  
Matches 349; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
QY 440 GCGGTTCCGAGAGTGTGATGATCAGGTGAGAGTGGCTCCAGAGTGGAGCTGTGAGATCTG 499  
DB 392 GGGTTTCTCGTGTCTCTTTTAAGAGGATCCAGTGTGAGGTGAGCTGTGAGATCTG 333  
QY 500 GGGGAGCGGTGTGCTCAGCCTGGAGAGTCCCTGAGACTCTCTGTGAGAGCTCTGATTC 559  
DB 332 GGGGAGCGGTGTGCTCAGCCTGGAGAGTCCCTGAGACTCTCTGTGAGAGCTCTGATTC 273  
QY 560 CCTTCAGAGCTTTGCTATGATGATGAGAGCTTAATTAATTAATTAATTAATTAATTAATTA 619  
DB 272 CCTTCAGAGCTTTGCTATGATGATGAGAGCTTAATTAATTAATTAATTAATTAATTAATTA 213  
QY 620 TGGCAGTTAT 679  
DB 212 TGGCAGTTAT 153  
QY 680 TCACCATCTCCAGAGACACTTCCAGAGACACGCTGTATCTTAAATTAATTAATTAATTAATTA 739  
DB 152 TCACCATCTCCAGAGACACTTCCAGAGACACGCTGTATCTTAAATTAATTAATTAATTAATTA 93  
QY 740 CTGAGAGACACGCTGTAT 799  
DB 92 CTGAGAGACACGCTGTAT 33  
QY 800 ACTACTACGTTTGAAGCTGTGGGGAAGG 830  
DB 32 ACTACTACGTTTGAAGCTGTGGGGAAGG 2

RESULT 11  
US-09-472-087-61

Sequence 61, Application US/09472087  
Patent No. 6682736  
GENERAL INFORMATION:  
APPLICANT: HANSON, DOUGLAS C.  
APPLICANT: NEVEU, MARK J.  
APPLICANT: MUELLER, EILEEN B.  
APPLICANT: HANKE, JEFFREY H.  
APPLICANT: GILMAN, STEVEN C.  
APPLICANT: DAVIS, C. GEOFFREY  
APPLICANT: CORVALAN, JOSE R.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
FILE REFERENCE: ABX-PFI  
CURRENT APPLICATION NUMBER: US/09/472,087  
PRIORITY FILING DATE: 1999-12-23  
PRIORITY FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 61  
LENGTH: 1413  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-472-087-61

Query Match 34.8%; Score 319.8; DB 4; Length 1413;  
Best Local Similarity 85.2%; Pred. No. 2.8e-81;  
Matches 357; Conservative 0; Mismatches 62; Indels 0; Gaps 0;  
QY 440 GCGGTTCCGAGAGTGTGATGATGAGTGTGCTCCAGAGTGGAGCTGTGAGATCTG 499  
DB 20 GGGTTTCTCGTGTCTCTTTTAAGAGGATCCAGTGTGAGGTGAGCTGTGAGATCTG 79  
QY 500 GGGGAGCGGTGTGCTCAGCCTGGAGAGTCCCTGAGACTCTCTGTGAGAGCTCTGATTC 559  
DB 80 GGGGAGCGGTGTGCTCAGCCTGGAGAGTCCCTGAGACTCTCTGTGAGAGCTCTGATTC 139  
QY 560 CCTTCAGAGCTTTGCTATGATGATGAGAGCTTAATTAATTAATTAATTAATTAATTAATTA 619  
DB 140 CCTTCAGAGCTTTGCTATGATGATGAGAGCTTAATTAATTAATTAATTAATTAATTAATTA 199  
QY 620 TGGCAGTTAT 679  
DB 200 TGGCAGTTAT 259  
QY 680 TCACCATCTCCAGAGACACTTCCAGAGACACGCTGTATCTTAAATTAATTAATTAATTAATTA 739  
DB 260 TCACCATCTCCAGAGACACTTCCAGAGACACGCTGTATCTTAAATTAATTAATTAATTAATTA 319  
QY 740 CTGAGAGACACGCTGTAT 799  
DB 320 CTGAGAGACACGCTGTAT 379  
QY 800 ACTACTACGTTTGAAGCTGTGGGGAAGG 830  
DB 380 ACTACTACGTTTGAAGCTGTGGGGAAGG 438

RESULT 12  
US-08-591-632-43  
Sequence 43, Application US/08591632  
Patent No. 6261558  
GENERAL INFORMATION:  
APPLICANT: Barbas, Carlos F.  
APPLICANT: Burton, Dennis R.  
APPLICANT: Lerner, Richard A.  
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL  
TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8  
CITY: La Jolla

STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/591,632  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/11907  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/308,841  
FILING DATE: 19-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/233,619  
FILING DATE: 26-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/139,409  
FILING DATE: 19-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 332.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937  
TELEFAX: (619) 784-9399  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4691 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
US-08-591-632-43

Query Match 34.7%; Score 318.4; DB 3; Length 4691;  
Best Local Similarity 88.4%; Pred. No. 1.2e-80;  
Matches 375; Conservative 0; Mismatches 31; Indels 18; Gaps 2;  
QY 7 ATGAAAAAACCGCTATGCCGATCGGATGTCAGTGGCTGGTTGCGCTACCGTTGGCGAG 66  
DB 2611 ATGAAAAAACAGCTATCGGATGTCAGTGGCTGGTTGCGCTACCGTTGGCGAG 2670  
QY 67 GCCGATATTGTGTGACGAGTCTCCAGGACCCCTGTTTGTCTCCAGGGGAAAGAGCC 126  
DB 2671 GCGG---CCGAGCTACGAGTCTCCAGGACCCCTGTTTGTCTCCAGGGGAAAGAGCC 2727  
QY 127 ACCCTCTCTGAGGCGGCGAGTCAGAGTGTAGTAGCAGTACTAGCCTGTGTACGAGCAG 186  
DB 2728 ACCCTCTCTGAGGCGGCGAGTCAGAGTGTAGTAGCAGTACTAGCCTGTGTACGAGCAG 2787  
QY 187 AAACCTGGCCAGGCTCCAGGCTCCTCATCTATGTGTGATCCACCAAGGGCCACTGGCAGT 246  
DB 2788 AAACCTGGCCAGGCTCCAGGCTCCTCATCTATGTGTGATCCACCAAGGGCCACTGGCAGT 2847  
QY 247 CCAGACAGGTCAGTGGCAGTGGGTCCGGGACAGACCTTCACTCTACCATCAGTGAAGT 306  
DB 2848 CCAGACAGGTCAGTGGCAGTGGGTCCGGGACAGACCTTCACTCTACCATCAGTGAAGT 2907  
QY 307 GAGCTGAAGATTTTGGCAGTGTATTACTGTACAGAGTATGTAGTACTCAGCTCAGACACT 366  
DB 2908 GAGCTGAAGATTTTGGCAGTGTATTACTGTACAGAGTATGTAGTACTCAGCTCAGACACT 2961  
QY 367 CAGATCATTTCGGGAGGAGCAAGAGTGTAGATCAAGCAAGTGTGGCTCAGCATTCT 426  
DB 2962 -----TTGCGCCAAAGGAGCAAGAGTGTAGATCAAGCAAGTGTGGCTCAGCATTCT 3012  
QY 427 GTCT 430  
|||||

DB 3013 GTCT 3016  
RESULT 13  
US-09-611-451-43  
Sequence 43, Application US/09611451  
Patent No. 6395275  
GENERAL INFORMATION:  
APPLICANT: Barbas, Carlos F.  
Lerner, Dennis R.  
Burton, Dennis R.  
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL  
ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
Patent Counsel  
STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/611,451  
FILING DATE: 06-Jul-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/591,632  
FILING DATE: 2001-10-29  
APPLICATION NUMBER: US 08/308,841  
FILING DATE: 19-SEP-1994  
APPLICATION NUMBER: US 08/233,619  
FILING DATE: 26-APR-1994  
APPLICATION NUMBER: US 08/139,409  
FILING DATE: 19-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 332.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937  
TELEFAX: (619) 784-9399  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4691 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
US-09-611-451-43  
Query Match 34.7%; Score 318.4; DB 3; Length 4691;  
Best Local Similarity 88.4%; Pred. No. 1.2e-80;  
Matches 375; Conservative 0; Mismatches 31; Indels 18; Gaps 2;  
QY 7 ATGAAAAAACCGCTATGCCGATCGGATGTCAGTGGCTGGTTGCGCTACCGTTGGCGAG 66  
DB 2611 ATGAAAAAACAGCTATCGGATGTCAGTGGCTGGTTGCGCTACCGTTGGCGAG 2670  
QY 67 GCCGATATTGTGTGACGAGTCTCCAGGACCCCTGTTTGTCTCCAGGGGAAAGAGCC 126  
DB 2671 GCGG---CCGAGCTACGAGTCTCCAGGACCCCTGTTTGTCTCCAGGGGAAAGAGCC 2727  
QY 127 ACCCTCTCTGAGGCGGCGAGTCAGAGTGTAGTAGCAGTACTAGCCTGTGTACGAGCAG 186  
DB 2728 ACCCTCTCTGAGGCGGCGAGTCAGAGTGTAGTAGCAGTACTAGCCTGTGTACGAGCAG 2787  
QY 187 AAACCTGGCCAGGCTCCAGGCTCCTCATCTATGTGTGATCCACCAAGGGCCACTGGCAGT 246

Db 2788 AAACCTGGCCAGGCTCCAGGCTCTCATCTATGATGATCCAGACAGGCGCACCTGCATC 2847  
QY 247 CCAGACAGGTTCACTGAGTGGTCCGAGACAGACTTCACTCCACCATCAGTACACTG 306  
Db 2848 CCAACAGAGTTCACTGAGTGGTCTGGACACACTTCACTCCACCATCAGTACACTG 2907  
QY 307 GAGCTGAAGATTTTGCAGTGTATTACTGTCCAGAGTATGGTACCTCACTCAGACACT 366  
Db 2908 GAGCTGAAGATTTTGCAGTGTATTACTGTCCAGAGTATGGTACCTCACTCAGTGTG 2961  
QY 367 CAGATCACTTTCGCGAGGAGCCAGAGTGGAGATCAAGAACTGTGCTGACACACT 426  
Db 2962 -----TTGCGCCAGAGGACCAAGGTGAACTCAAGAACTGTGCTGACACACT 3012  
QY 427 GTCT 430  
Db 3013 GTCT 3016

RESULT 14  
US-08-591-632-51  
Sequence 51, Application US/08591632  
Patent No. 6261558  
GENERAL INFORMATION:  
APPLICANT: Barbás, Carlos F.  
APPLICANT: Burton, Dennis R.  
APPLICANT: Lerner, Richard A.  
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
Patent Counsel  
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/591,632  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/11907  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/308,841  
FILING DATE: 19-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/233,619  
FILING DATE: 26-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/139,409  
FILING DATE: 19-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 332.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937  
TELEFAX: (619) 784-9399  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6166 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)

US-08-591-632-51  
Query Match 34.7%; Score 318.4; DB 3; Length 6166;  
Best Local Similarity 88.4%; Pred. No. 1.4e-80;  
Matches 375; Conservative 0; Mismatches 31; Indels 18; Gaps 2;  
QY 7 ATGAAAAAACCGCTATCGCGATCCGAGTTGACCTGGCTGTTGGCTACCGTTGCGCAG 66  
Db 4541 ATGAAAAAACCGCTATCGCGATCCGAGTTGACCTGGCTGTTGGCTACCGTTGCGCAG 4600  
QY 67 GCGATATTGTGTGACGAGTCTCAGGCACTCTGTCTTGTCTCCAGGGGAAAGAGCC 126  
Db 4601 GCGG---CCGACTACGAGAGTCTCAGGCACTCTGTCTTGTCTCCAGGGGAAAGAGCC 4657  
QY 127 ACCCTCTCTGCGAGGCGCAGTCAAGTGTATGACAGCTACTTAAGCTGTGACGAGC 186  
Db 4658 ACCCTCTCTGCGAGGCGCAGTCAAGTGTATGACAGGCGCTACTTAAGCTGTGACGAGC 4717  
QY 187 AAACCTGGCCAGGCTCCAGGCTCTCATCTATGATGATCCAGACAGGCGCACCTGCATG 246  
Db 4718 AAACCTGGCCAGGCTCCAGGCTCTCATCTATGATGATCCAGACAGGCGCACCTGCATG 4777  
QY 247 CCAGACAGGTTCACTGAGTGGTCCGAGACAGACTTCACTCCACCATCAGTACACTG 306  
Db 4778 CCAACAGAGTTCACTGAGTGGTCTGGACACACTTCACTCCACCATCAGTACACTG 4837  
QY 307 GAGCTGAAGATTTTGCAGTGTATTACTGTCCAGAGTATGGTACCTCACTCAGACACT 366  
Db 4838 GAGCTGAAGATTTTGCAGTGTATTACTGTCCAGAGTATGGTACCTCACTCAGACACT 4891  
QY 367 CAGATCACTTTCGCGAGGAGCCAGAGTGGAGATCAAGAACTGTGCTGACACACT 426  
Db 4892 -----TTGCGCCAGAGGACCAAGGTGAACTCAAGAACTGTGCTGACACACT 4942  
QY 427 GTCT 430  
Db 4943 GTCT 4946

RESULT 15  
US-09-611-451-51  
Sequence 51, Application US/09611451  
Patent No. 6395275  
GENERAL INFORMATION:  
APPLICANT: Barbás, Carlos F.  
APPLICANT: Burton, Dennis R.  
APPLICANT: Lerner, Richard A.  
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
Patent Counsel  
STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/611,451  
FILING DATE: 06-JUL-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/591,632  
FILING DATE: 2001-10-29  
APPLICATION NUMBER: US 08/308,841  
FILING DATE: 19-SEP-1994  
APPLICATION NUMBER: US 08/233,619  
FILING DATE: 26-APR-1994

APPLICATION NUMBER: US 08/139,409  
FILING DATE: 19-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Filting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 332.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937  
TELEFAX: (619) 784-9399  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6166 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-09-611-451-51

Query Match 34.7%; Score 318.4; DB 3; Length 6166;  
Best Local Similarity 88.4%; Pred. No. 1.4e-80;  
Matches 375; Conservative 0; Mismatches 31; Indels 18; Gaps 2;  
QY 7 ATGAAAAAACCGCTATCGCGATGCGAGTGTGCACTGGCTGGTTGGTACCGGTGGCGCAG 66  
DB 4541 ATGAAAAAGACAGCTATCGCGATGCGAGTGTGCACTGGCTGGTTGGTACCGGTGGCGCAG 4600  
QY 67 GCGGATATTGTGTGACGAGTCTCCAGGCAACCCTGTCTTTGTCTCCAGGGGAAAGAGCC 126  
DB 4601 GCGG---CCGAGCTACGCGAGTCTCCAGGCAACCCTGTCTTTGTCTCCAGGGGAAAGAGCC 4657  
QY 127 ACCCTCTCTGCAAGGCGCAGTCAAGAGTGTAGTACGAGTACTTACCTGTGTACAGCAG 186  
DB 4658 ACCCTCTCTGCAAGGCGCAGTCAAGAGTGTAGTACGAGGCTTACTTACCTGTGTACAGCAG 4717  
QY 187 AAACCTGGCCAGGCTCCAGGCTCCATCTATGTGTGATCCAGCCAGGGGCCACTGGCATG 246  
DB 4718 AAACCTGGCCAGGCTCCAGGCTCCATCTATGTGTGATCCAGCCAGGGGCCACTGGCATG 4777  
QY 247 CCAGACAGGTTCAAGTGGCAAGTGGTCCGGGACAGACTTCATCTCACCATCAGTAGACTG 306  
DB 4778 CCAGACAGGTTCAAGTGGCAAGTGGTCCGGGACAGACTTCATCTCACCATCAGTAGACTG 4837  
QY 307 GAGCTTGAAGATTTTGCAGTGTATTAATGTCTCAGCAGTATGTAGTCACTCACTCAGACACT 366  
DB 4838 GAGCTTGAAGATTTTGCAGTGTATTAATGTCTCAGCAGTATGTAGTCACTCACTCAGACACT 4891  
QY 367 CAGATCACTTTGGGGGAGGAGCAAGAGTGGAGATCAAGCAACTGTGGCTGCACCATCT 426  
DB 4892 -----TTGGGCCAAGGAGCAAGAGTGGAGATCAAGCAACTGTGGCTGCACCATCT 4942  
QY 427 GTCT 430  
DB 4943 GTCT 4946

Search completed: February 18, 2005, 08:27:53  
Job time : 207 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 05:58:59 ; Search time 653 Seconds

(without alignments)  
8309.090 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 918  
Sequence: 1 GAATTCATGAAAAAAGCCG.....ATCACCATTGTAAGCTT 918

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	918	100.0	918	10	US-09-782-397-13
2	918	100.0	918	17	US-10-651-453-13
3	916.4	99.8	918	10	US-09-782-397-15
4	916.4	99.8	918	17	US-10-651-453-15
5	799.6	87.1	867	17	US-09-782-397-16
6	799.6	87.1	867	17	US-10-651-453-16
7	798	86.9	867	10	US-09-782-397-18
8	798	86.9	867	17	US-10-651-453-18
9	395.2	43.1	840	17	US-10-409-938-20
10	361	39.3	450	10	US-09-782-397-6
11	361	39.3	450	17	US-10-651-453-6

12	359.4	39.2	450	10	US-09-782-397-4	Sequence 4, Appl1
13	359.4	39.2	450	17	US-10-651-453-4	Sequence 4, Appl1
14	337.8	36.7	762	17	US-10-423-847-8	Sequence 8, Appl1
15	336.8	36.7	741	17	US-10-423-847-4	Sequence 4, Appl1
16	336.8	36.7	756	17	US-10-423-847-1	Sequence 1, Appl1
17	336.8	36.7	759	17	US-10-423-847-2	Sequence 2, Appl1
18	335.2	35.5	756	17	US-10-423-847-5	Sequence 5, Appl1
19	325.4	35.4	543	17	US-10-651-453-1	Sequence 1, Appl1
20	325.4	35.4	543	17	US-10-651-453-3	Sequence 3, Appl1
21	324.4	35.3	543	10	US-09-782-397-1	Sequence 1, Appl1
22	324.4	35.3	543	10	US-09-782-397-3	Sequence 3, Appl1
23	324.2	35.3	1539	18	US-10-492-729-4	Sequence 4, Appl1
24	324.2	35.3	1539	18	US-10-492-729-12	Sequence 12, Appl1
25	319.8	34.8	1413	14	US-10-153-382-16	Sequence 16, Appl1
26	319.8	34.8	1413	18	US-10-612-497-51	Sequence 61, Appl1
27	319.8	34.8	1413	18	US-10-776-649-61	Sequence 61, Appl1
28	318.2	34.7	1413	17	US-10-292-088-77	Sequence 77, Appl1
29	316.6	34.5	1413	17	US-10-292-088-61	Sequence 61, Appl1
30	315.2	34.3	376	17	US-10-292-088-73	Sequence 73, Appl1
31	314.2	34.2	487	17	US-10-395-894-30	Sequence 30, Appl1
32	314.2	34.2	487	18	US-10-695-667-30	Sequence 30, Appl1
33	314.2	34.2	7576	17	US-10-395-894-6	Sequence 6, Appl1
34	314.2	34.2	7576	18	US-10-695-667-6	Sequence 6, Appl1
35	312.6	34.1	420	18	US-10-714-353-3	Sequence 3, Appl1
36	312.6	34.1	421	18	US-10-714-353-11	Sequence 11, Appl1
37	312	34.0	376	17	US-10-292-088-57	Sequence 57, Appl1
38	310.8	33.9	2011	18	US-10-684-109-80	Sequence 80, Appl1
39	310.8	33.9	2011	18	US-10-684-109-81	Sequence 81, Appl1
40	310.6	33.8	678	10	US-09-453-234-49	Sequence 49, Appl1
41	310.6	33.8	678	10	US-09-453-234-85	Sequence 85, Appl1
42	309.4	33.7	1450	17	US-10-291-265-568	Sequence 568, App
43	309.4	33.7	1450	17	US-10-291-265-569	Sequence 569, App
44	309.4	33.7	1450	17	US-10-291-265-570	Sequence 570, App
45	309.4	33.7	1450	17	US-10-291-265-571	Sequence 571, App

#### ALIGNMENTS

RESULT 1  
US-09-782-397-13  
Sequence 13, Application US/09782397 + *Approved*  
Publication No. US20030021779A1  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
Kaplan, Pradipt K.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.

1	REGISTRATION NUMBER: 33,943	
2	REFERENCE/DOCKET NUMBER: 31608-20001.20	
3	TELECOMMUNICATION INFORMATION:	
4	TELEPHONE: (650) 813-5600	
5	TELEFAX: (650) 494-0792	
6	TELEX: 706141	
7	INFORMATION FOR SEQ ID NO: 13:	
8	SEQUENCE CHARACTERISTICS:	
9	LENGTH: 918 base pairs	
10	TYPE: nucleic acid	
11	STRANDEDNESS: single	
12	TOPOLOGY: linear	
13	FEATURE:	
14	NAME/KEY: CDS	
15	LOCATION: join(1..906, 913..918)	
16	SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
17	US-09-782-357-13	
18	Query Match	100.0%; Score 918; DB 10; Length 918;
19	Best Local Similarity	100.0%; Pred. No. 3.2e-274;
20	Matches	918; Conservative 0; Mismatches 0; Indels 0; Gaps 0
21	1	GAATTCATGAAAAAACCGCTATCGCGATCGGAGATTGCACTGCGCTGTTCCGTACCGTT
22	1	GAATTCATGAAAAAACCGCTATCGCGATCGGAGATTGCACTGCGCTGTTCCGTACCGTT
23	61	CGCGAGGCGGATATTGTGTGTTGACGAGCTCCAGGACCCCTGTCTTGTCTCCAGGGAA
24	61	GCGCAGGCGGATATTGTGTGTTGACGAGCTCCAGGACCCCTGTCTTGTCTCCAGGGAA
25	121	AGAGCCACCTCTCTCTGCGAGGGCCAGTCAAGTGTGTTAGTACGACTCTTACCTGTATC
26	121	AGAGCCACCTCTCTCTGCGAGGGCCAGTCAAGTGTGTTAGTACGACTCTTACCTGTATC
27	181	CAGCAGAAACCTGGCGAGGCTCCAGGCTCCATCTATATGTAGTATCCACAGGGCACT
28	181	CAGCAGAAACCTGGCGAGGCTCCAGGCTCCATCTATATGTAGTATCCACAGGGCACT
29	241	GCGATGCGAGACAGGTTCAGTGGCAGTGGGTCGGGACAGACTTCACTCTCAACCATCACT
30	241	GCGATGCGAGACAGGTTCAGTGGCAGTGGGTCGGGACAGACTTCACTCTCAACCATCACT
31	301	AGACTGAGGCTGAGATTTTGCAAGTATTTACTGACAGATATGTATGATCACTCCAG
32	301	AGACTGAGGCTGAGATTTTGCAAGTATTTACTGACAGATATGTATGATCACTCCAG
33	361	ACACCTCAGATCACTTTCGGCGAGGAGACCAAGGTGAGATCAACGAACTGTGCTGCA
34	361	ACACCTCAGATCACTTTCGGCGAGGAGACCAAGGTGAGATCAACGAACTGTGCTGCA
35	421	CCATCTGTCTCTGCGCGGTGGCGGTTCCGAGGTGTTGATCAAGTGTGAGTGTGCTCCAG
36	421	CCATCTGTCTCTGCGCGGTGGCGGTTCCGAGGTGTTGATCAAGTGTGAGTGTGCTCCAG
37	481	GTGCACTGTGTGAGTCTGTGGGAGAGCGGTGTCAGACTGGAGAGTCCCTGAGACTCTCC
38	481	GTGCACTGTGTGAGTCTGTGGGAGAGCGGTGTCAGACTGGAGAGTCCCTGAGACTCTCC
39	541	TGTGAGCCTCTGATTCCTCCCTTCAGAAAGCTTGTCTATGCACTGGGTCCGCAAGGCTCA
40	541	TGTGAGCCTCTGATTCCTCCCTTCAGAAAGCTTGTCTATGCACTGGGTCCGCAAGGCTCA
41	601	GCGAAGGGGCTGAGTGTGGTGGCAGTTATATATATGATGAGGAACCTAAATCTACGCA
42	601	GCGAAGGGGCTGAGTGTGGTGGCAGTTATATATATGATGAGGAACCTAAATCTACGCA
43	661	GACTCCGTGAGAGGCGATTCAACAATTCAGAGCACTTCCAAAGAACGGGTATCTTA
44	661	GACTCCGTGAGAGGCGATTCAACAATTCAGAGCACTTCCAAAGAACGGGTATCTTA
45	721	AAATGAAACGCTTGAACCTGAGACAGGCTGTATTAATCTGTGCGAGAGATCAGAGC
46	721	AAATGAAACGCTTGAACCTGAGACAGGCTGTATTAATCTGTGCGAGAGATCAGAGC

OY		781	CCTGGGAGACATATACA	CGACTA	CGGTTCGA	CGTCTGGGGCAAA	GAGGCAC	CGGTC	840
DB		781	CTGTGGGAGACTATATA	CCACTACTAC	GGTTTGAC	CGTGGGCAAA	GAGGCAC	CGGTC	840
OY		841	ACCGTCTCCTCAGATCC	GCAGAACAAA	CTGATCAG	CGGAGAAGATCT	GAACCATCACCAT	900	
DB		841	ACCGTCTCCTCAGATCC	GCAGAACAAA	CTGATCAG	CGGAGAAGATCT	GAACCATCACCAT	900	
OY		901	CACCATTAGTGAAGCTT	918					
DB		901	CACCATTAGTGAAGCTT	918					
 RESULT 2 US-10-651-453-13 Sequence 13, Application US/10651453 Publication No. US20040091484A1 GENERAL INFORMATION: APPLICANT: Dan, Michael D. APPLICANT: Maif, Pradip K. TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS. TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHETIC FILE REFERENCE: 316082000103 CURRENT APPLICATION NUMBER: US/10/651,453 CURRENT FILING DATE: 2003-08-29 PRIOR APPLICATION NUMBER: US 09/782,397 PRIOR FILING DATE: 2001-02-13 PRIOR APPLICATION NUMBER: US 08/862,124 PRIOR FILING DATE: 1997-05-22 PRIOR APPLICATION NUMBER: US 08/657,449 PRIOR FILING DATE: 1996-05-22 NUMBER OF SEQ ID NOS: 29 SOFTWARE: PatentIn version 3.1 SEQ ID NO 13 LENGTH: 918 TYPE: DNA ORGANISM: Homo Sapiens NAME/KEY: CDS LOCATION: (1)..(906) OTHER INFORMATION: FEATURE: NAME/KEY: CDS LOCATION: (913)..(918) OTHER INFORMATION: US-10-651-453-13									
 Query Match                      100.0%; Score 918; DB 17; Length 918; Best Local Similarity    100.0%; Pred. No. 3,2e-274; Matches 918; Conservative    0; Mismatches    0; Indels    0; Gaps    0;									
OY		1	GAATTCATGAAAAAA	CCGCTATCGCATG	CGAGTTGC	ACTGGCTGGTTG	CGCTACCGTT	60	
DB		1	GAATTCATGAAAAAA	CCGCTATCGCATG	CGAGTTGC	ACTGGCTGGTTG	CGCTACCGTT	60	
OY		61	GGCGAAGCCGATATT	TGGTTGAGCGAGT	CTCCAGGAC	CCGTCTTGTCT	CCAGGGGAA	120	
DB		61	GGCGAAGCCGATATT	TGGTTGAGCGAGT	CTCCAGGAC	CCGTCTTGTCT	CCAGGGGAA	120	
OY		121	AGAGCACCCTCTCT	CGACGGGCGAGT	CAGAGTGT	ATTAGACAG	AGCTTAAGCTTG	180	
DB		121	AGAGCACCCTCTCT	CGACGGGCGAGT	CAGAGTGT	ATTAGACAG	AGCTTAAGCTTG	180	
OY		181	CAGCAGAAACCTG	GCCAGGCTCC	CAGGCTCCT	CACTATATG	TGTCATCC	ACGAGGCCACT	240
DB		181	CAGCAGAAACCTG	GCCAGGCTCC	CAGGCTCCT	CACTATATG	TGTCATCC	ACGAGGCCACT	240
OY		241	GGATATCCGACAG	AGTTCAAGTGG	CGAGTGGGT	CCGGGACAG	ACTTCACTTC	CAATCAGT	300
DB		241	GGATATCCGACAG	AGTTCAAGTGG	CGAGTGGGT	CCGGGACAG	ACTTCACTTC	CAATCAGT	300



301 AGACTGAGCCTGAAAGATTGTCAGTATCTGTCAGAGATGTAAGTCACTCAG 360  
301 AGACTGAGCCTGAAAGATTGTCAGTATCTGTCAGAGATGTAAGTCACTCAG 360  
361 ACACCTCAGATCACTTTCGCGAGAGGAGCAAGGTGAGATCAAGCAAGTGTGCTGA 420  
361 ACACCTCAGATCACTTTCGCGAGAGGAGCAAGGTGAGATCAAGCAAGTGTGCTGA 420  
421 CCATCTGTCTTGGCGGTCGCGGTTCCGAGGTGTGATCAGGTGAGGTGCTCCAG 480  
421 CCATCTGTCTTGGCGGTCGCGGTTCCGAGGTGTGATCAGGTGAGGTGCTCCAG 480  
481 GTGCAAGCTGTGAGTCTGCGGAGGAGGCTGTGATCAGCTGAGGTCCTGAGACTTC 540  
481 GTGCAAGCTGTGAGTCTGCGGAGGAGGCTGTGATCAGCTGAGGTCCTGAGACTTC 540  
541 TGTGCAAGCTGTGATTCCTTCAGAGCTTGTATGCACTGGGTCGCGAGCTCTA 600  
541 TGTGCAAGCTGTGATTCCTTCAGAGCTTGTATGCACTGGGTCGCGAGCTCTA 600  
601 GGCAGAGGCTGTGAGTGTGCGGTCGAGTTATATCATATGATGAGCACTAATATCA 660  
601 GGCAGAGGCTGTGAGTGTGCGGTCGAGTTATATCATATGATGAGCACTAATATCA 660  
661 GACTCGGTGAAGGGCCGATTCACATCTCCAGAGACACTTCCAGAAACGCGTATCTA 720  
661 GACTCGGTGAAGGGCCGATTCACATCTCCAGAGACACTTCCAGAAACGCGTATCTA 720  
721 AAAATGACAGCCTGAGAACTGAGACAGCGCTGTATATCTATGTCGAGAGATCAGAG 780  
721 AAAATGACAGCCTGAGAACTGAGACAGCGCTGTATATCTATGTCGAGAGATCAGAG 780  
781 CTGTTGGTGTATGATGACCACTAATCGTTTGAAGTCTGGGCAAGGAGCAAGCTC 840  
781 CTGTTGGTGTATGATGACCACTAATCGTTTGAAGTCTGGGCAAGGAGCAAGCTC 840  
841 ACCGTCCTCAGATCCGAGCAAAAGATGATGAGGAGAGATGTAACCATCACT 900  
841 ACCGTCCTCAGATCCGAGCAAAAGATGATGAGGAGAGATGTAACCATCACT 900  
901 CACCATTAAGTGAAGCTT 918  
901 CACCATTAAGTGAAGCTT 918

RESULT 3  
US-09-782-397-15/c  
Sequence 15, Application US/09782397  
Publication No. US2003002179A1  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
Maici, Pradip K.  
Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT  
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397

FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 918 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-782-397-15  
Query Match 99.8%; Score 916.4; DB 10; Length 918;  
Best Local Similarity 99.9%; Pred. No. 1e-273;  
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 GAATTCATGAAAAAACCCTATTCGGATCGAGTTGCACTGGCTGTTCCGTACCGTT 60  
918 GAATTCATGAAAAAACCCTATTCGGATCGAGTTGCACTGGCTGTTCCGTACCGTT 859  
61 GGGCAGGCGGATTTGTGTGACAGAGTCTCCAGAGCACTGCTTGTGTCTCAAGGGA 120  
858 GGGCAGGCGGATTTGTGTGACAGAGTCTCCAGAGCACTGCTTGTGTCTCAAGGGA 799  
121 AGAGCAACCTCTCTGTCAGAGGCGAGTCAAGAGTGTAGAGCACTTAAAGCTGTAC 180  
798 AGAGCAACCTCTCTGTCAGAGGCGAGTCAAGAGTGTAGAGCACTTAAAGCTGTAC 739  
181 CAGCAAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGATGATCAACAGGCGCACT 240  
738 CAGCAAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGATGATCAACAGGCGCACT 679  
241 GGCATGCCAGAGAGTTGATGAGTGGTCCGAGAGCAAGATCTTCACTCACTCACT 300  
678 GGCATGCCAGAGAGTTGATGAGTGGTCCGAGAGCAAGATCTTCACTCACTCACT 619  
301 AGACTGAGCCTGAAAGATTGTCAGTATCTGTCAGAGATGTAAGTCACTCAG 360  
618 AGACTGAGCCTGAAAGATTGTCAGTATCTGTCAGAGATGTAAGTCACTCAG 559  
361 ACACCTCAGATCACTTTCGCGAGAGGAGCAAGGTGAGATCAAGCAAGTGTGCTGA 420  
558 ACACCTCAGATCACTTTCGCGAGAGGAGCAAGGTGAGATCAAGCAAGTGTGCTGA 499  
421 CCATCTGTCTTGGCGGTCGCGGTTCCGAGGTGTGATCAGGTGAGGTGCTCCAG 480  
498 CCATCTGTCTTGGCGGTCGCGGTTCCGAGGTGTGATCAGGTGAGGTGCTCCAG 439  
481 GTGCAAGCTGTGAGTCTGCGGAGGAGGCTGTGATCAGCTGAGGTCCTGAGACTTC 540  
438 GTGCAAGCTGTGAGTCTGCGGAGGAGGCTGTGATCAGCTGAGGTCCTGAGACTTC 379  
541 TGTGCAAGCTGTGATTCCTTCAGAGCTTGTATGCACTGGGTCGCGAGCTCTA 600  
378 TGTGCAAGCTGTGATTCCTTCAGAGCTTGTATGCACTGGGTCGCGAGCTCTA 319  
601 GGCAGAGGCTGTGAGTGTGCGGTCGAGTTATATCATATGATGAGCACTAATATCA 660  
318 GGCAGAGGCTGTGAGTGTGCGGTCGAGTTATATCATATGATGAGCACTAATATCA 259  
661 GACTCGGTGAAGGGCCGATTCACATCTCCAGAGACACTTCCAGAAACGCGTATCTA 720  
258 GACTCGGTGAAGGGCCGATTCACATCTCCAGAGACACTTCCAGAAACGCGTATCTA 199

OY		721	AAAAAAGAACGGCTGACGAATCTGAGCAACCGCTGTCTTACTGTGCAGAGATCAAGC	780
Db		198	AAAAGAACAAGCTTGAAACTGAGACACCGCTGTCTTACTGTGCAGAGATCAAGC	139
OY		781	CTGTGGGTGACTATGACCATTACTACTGAGTTCGTTGACGTCCTGGGCAAAAGGACACGGTC	840
Db		138	CTGTGGGTGACTATGACCATTACTACTGAGTTCGTTGACGTCCTGGGCAAAAGGACACGGTC	79
OY		841	ACCGTCTCTCAAGATCCGAAACAAAACTGANTCACCGAAGAAAGATCTGAACCATCAAGAT	900
Db		78	ACCGTCTCTCAAGATCCGAAACAAAACTGANTCACCGAAGAAAGATCTGAACCATCAAGAT	19
OY		901	CACCATTAGTGAAAGCTT	918
Db		18	CACCATTAGTGAAAGCTT	1
 RESULT 4 US-10-651-453-15/c ; Sequence 15, Application US/10651453 ; Publication No. US20040091484A1 ; GENERAL INFORMATION: ; APPLICANT: Dan, Michael D. ; APPLICANT: Matli, Pradip K. ; APPLICANT: Kaplan, Howard A. ; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS, ; TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHETIC ; TITLE OF INVENTION: DETECTION OF CANCERS ; FIDE REFERENCE: 316082000103 ; CURRENT APPLICATION NUMBER: US/10/651,453 ; CURRENT FILING DATE: 2003-08-29 ; PRIOR APPLICATION NUMBER: US 09/782,397 ; PRIOR FILING DATE: 2001-02-13 ; PRIOR APPLICATION NUMBER: US 08/862,124 ; PRIOR FILING DATE: 1997-05-22 ; PRIOR APPLICATION NUMBER: US 08/657,449 ; PRIOR FILING DATE: 1996-05-22 ; NUMBER OF SEQ ID NOS: 29 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 15 ; LENGTH: 918 ; TYPE: DNA ; ORGANISM: Homo Sapiens US-10-651-453-15				
 Query Match            99.8%; Score 916.4; DB 17; Length 918; Best Local Similarity   99.9%; Pred. No. 1e-273; Matches   917; Conservative   0; Mismatches   1; Indels   0; Gaps   0;				
OY		1	GAATTCATGAAAAAAAAACCGCTATCGCGATGCGAGTTGACGTGGCTTGGCTACCGTT	60
Db		918	GAATTCATGAAAAAAAAACCGCTATCGCGATGCGAGTTGACGTGGCTTGGCTACCGTT	859
OY		61	GCGCAGGCCGANTATTGTGTGACGCAGTCTCCAGGCACTGTCTTGTCTCCAGGGAA	120
Db		858	GCGCAGGCCGANTATTGTGTGACGCAGTCTCCAGGCACTGTCTTGTCTCCAGGGAA	799
OY		121	AGAGCCACCTCTCTCTGACAGGGCCAGTCAGAGTGTTAATACAGTACTTACCTGTAC	180
Db		798	AGAGCCACCTCTCTCTGACAGGGCCAGTCAGAGTGTTAATACAGTACTTACCTGTAC	739
OY		181	CAGCAGAAACCTGGCAGAGCTCCAGGCTCTCATCTAATGGTGATCCACAGAGGCCACT	240
Db		738	CAGCAGAAACCTGGCAGAGCTCCAGGCTCTCATCTAATGGTGATCCACAGAGGCCACT	679
OY		241	GGCATGCCAGACAGGTTCAGTGGCAGTGGGATCCGGACAGACTTCACTCCACATCAGT	300
Db		678	GGCATGCCAGACAGGTTCAGTGGCAGTGGGATCCGGACAGACTTCACTCCACATCAGT	619
OY		301	AGACTGGAGCCTGAAGATTTTGGCACTGTATTACTGTACAGAGTATGGTAGCTCACTGAG	360
Db		618	AGACTGGAGCCTGAAGATTTTGGCACTGTATTACTGTACAGAGTATGGTAGCTCACTGAG	559

QY	361	ACACCTCAGATCACTTTGGGCGAGGACCAAGGTGAGATCAACAACTGTGGCTGCA	420
Db	558	ACACCTCAGATCACTTTGGGCGAGGACCAAGGTGAGATCAACAACTGTGGCTGCA	499
QY	421	CCATCTGTCTCTGGCGGTGGCGGTTCCGAGAGTGGTGAATCAAGTGGTGGCTCCAG	480
Db	498	CCATCTGTCTCTGGCGGTGGCGGTTCCGAGAGTGGTGAATCAAGTGGTGGCTCCAG	439
QY	481	GTGACAGCTGTGGAGTCTGGGGGGAAGCGGTGATCCAGCCTGGGAGGTCCCTGACCTCC	540
Db	438	GTGACAGCTGTGGAGTCTGGGGGGAAGCGGTGATCCAGCCTGGGAGGTCCCTGACCTCC	379
QY	541	TGTGACAGCTGTGATTTCCCTTCAGAACTTTGCTATGCACTGGGTCCGCCAGCTCTA	600
Db	378	TGTGACAGCTGTGATTTCCCTTCAGAACTTTGCTATGCACTGGGTCCGCCAGCTCTA	319
QY	601	GGCAAGGGGGCTGGAGTGGGTGGCGAGTTATATCATATGTATGATGGAAGCACTAATACTACGCA	660
Db	318	GGCAAGGGGGCTGGAGTGGGTGGCGAGTTATATCATATGTATGGAAGCACTAATACTACGCA	259
QY	661	GACCTCCGGAAGGGGCCATTTCCATCCATCCAGAGCACTTCCAGAAACAGCGGTGATCTA	720
Db	258	GACCTCCGGAAGGGGCCATTTCCATCCATCCAGAGCACTTCCAGAAACAGCGGTGATCTA	199
QY	721	AAATGGAACAGCTGAGAACTGAGGACACGGCTGTCTATTACTGTGCGAGAGATCAGAGC	780
Db	198	AAATGGAACAGCTGAGAACTGAGGACACGGCTGTCTATTACTGTGCGAGAGATCAGAGC	139
QY	781	CTGTTGGGTGACTATGACCACTACTACGCGTTTGGACGTCGTGGGGCAAAAGGACACAGCTC	840
Db	138	CTGTTGGGTGACTATGACCACTACTACGCGTTTGGACGTCGTGGGGCAAAAGGACACAGCTC	79
QY	841	ACCGTTCCTGAGGATCCGAACAAAACTGATCAGCGGAAGAAAGATCTGAACCATCAGCAT	900
Db	78	ACCGTTCCTGAGGATCCGAACAAAACTGATCAGCGGAAGAAAGATCTGAACCATCAGCAT	19
QY	901	CACCATTTAGTGAAGCTT 918	
Db	18	CACCATTTAGTGAAGCTT 1	
RESULT 5			
US-09-782-397-16			
; Sequence 16, Application US/09782397			
; Publication No. US2003002179A1			
GENERAL INFORMATION:			
APPLICANT: Dan, Michael D.			
Mailli, Pradip K.			
Kaplan, Howard A.			
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT			
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE			
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND			
DETECTION OF CANCERS			
NUMBER OF SEQUENCES: 28			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Morrison & Foerster LLP			
STREET: 755 Page Mill Road			
CITY: Palo Alto			
STATE: CA			
COUNTRY: USA			
ZIP: 94304-1018			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/782,397			
FILING DATE: 13-Feb-2001			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 08/862,124			

FILED DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 867 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1..855, 862..867)  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-782-397-16

Query Match 87.1%; Score 799.6; DB 10; Length 867;  
Best Local Similarity 94.0%; Pred. No. 1.8e-237;  
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

```
QY 1 GAATTCATGAAAAAACCCTATCGGATCGGATGGAAGTGGCTGGTTTCCTACCGTT 60
DB 1 GAATTCATGAAAAAACCCTATCGGATCGGATGGAAGTGGCTGGTTTCCTACCGTT 60
QY 61 GCGCAGCCGATATGTGTGAAGCAGTCTCCAGGACCCCTGTTGTCTCCAGGGAA 120
DB 61 GCGCAGCCGATATGTGTGAAGCAGTCTCCAGGACCCCTGTTGTCTCCAGGGAA 120
QY 121 AAGCCACCTCTCTCTGCAAGGCGAGTCAAGAGTTAGTAGAGCTTAAGCTGTGAC 180
DB 121 AAGCCACCTCTCTCTGCAAGGCGAGTCAAGAGTTAGTAGAGCTTAAGCTGTGAC 180
QY 121 AAGCCACCTCTCTCTGCAAGGCGAGTCAAGAGTTAGTAGAGCTTAAGCTGTGAC 180
DB 121 AAGCCACCTCTCTCTGCAAGGCGAGTCAAGAGTTAGTAGAGCTTAAGCTGTGAC 180
QY 181 CAGCAGAACTGGCCAGGCTCCAGGCTCCATCTATGTCAGTCCACACGAGGCACT 240
DB 181 CAGCAGAACTGGCCAGGCTCCAGGCTCCATCTATGTCAGTCCACACGAGGCACT 240
QY 241 GGCATGCCAGAGGTTGAGTGAAGTGGTCCGGACAGACTTCACTCAACATCACT 300
DB 241 GGCATGCCAGAGGTTGAGTGAAGTGGTCCGGACAGACTTCACTCAACATCACT 300
QY 301 AACTGAGACCTGAAAGATTTGAGTGAATTAAGTCAAGATGATGATCACTGAG 360
DB 301 AACTGAGACCTGAAAGATTTGAGTGAATTAAGTCAAGATGATGATCACTGAG 360
QY 361 AACTGAGATCACTTTCGCGAGAGGACCAAGTGAATCAAGAACTGTGGTGA 420
DB 361 AACTGAGATCACTTTCGCGAGAGGACCAAGTGAATCAAGAACTGTGGTGA 420
QY 421 CCATCTGTCCTGCGGTGGCGGTTCCGAGGTGTGATCAGTGAAGTGGTCCAG 480
DB 421 TC-----CGACAG 429
QY 481 GTGAGCTGTGAGTCTGCGGAGGCGGTGTCAGGCTGGAGGTCCTGAGACTTCC 540
DB 481 GTGAGCTGTGAGTCTGCGGAGGCGGTGTCAGGCTGGAGGTCCTGAGACTTCC 540
QY 541 TGTGAGCTCTGAGATTCCTTCAGAACTTGTGATGCACTGGGTCGCGAGGCTCA 600
DB 541 TGTGAGCTCTGAGATTCCTTCAGAACTTGTGATGCACTGGGTCGCGAGGCTCA 600
QY 601 GCGCAGGCGCTGAGTGTGAGTGAATATATGATGAAGCACTAAATACTAGCA 660
DB 601 GCGCAGGCGCTGAGTGTGAGTGAATATATGATGAAGCACTAAATACTAGCA 660
QY 661 GACTCCGTGAGAGGCGGATTCACCATCTCCAGAGACCTTCCAGAAACGGTGTATCTA 720
DB 661 GACTCCGTGAGAGGCGGATTCACCATCTCCAGAGACCTTCCAGAAACGGTGTATCTA 720
```

```
QY 721 AAATGAACAGCTGAGAACTGAGACAGCGCTGTATTAATGTCGAGATCAGAGC 780
DB 670 AAATGAACAGCTGAGAACTGAGACAGCGCTGTATTAATGTCGAGATCAGAGC 729
QY 781 CTGTTGGTGAATGACCACTACTACGTTTGAAGTGTGGGCAAGAGGACGAGTC 840
DB 730 CTGTTGGTGAATGACCACTACTACGTTTGAAGTGTGGGCAAGAGGACGAGTC 789
QY 841 ACCGTCCTCAGAGATCCGAAACAAAACATGATCAGGAGAAAGATGTGAACCTACCAT 900
DB 790 ACCGTCCTCAGAGATCCGAAACAAAACATGATCAGGAGAAAGATGTGAACCTACCAT 849
QY 901 CACCATTAAGTGAAGCTT 918
DB 850 CACCATTAAGTGAAGCTT 867

RESULT 6
US-10-651-453-16
; Sequence 16, Application US/10651453
; Publication No. US20040091464A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maici, Pradiip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS.
; TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PRO:
; FILE REFERENCE: 31608200103
; CURRENT APPLICATION NUMBER: US/10/651,453
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 09/782,397
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 08/862,124
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: US 08/657,449
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Homo Sapiens
; NAME/KEY: CDS
; LOCATION: (1)..(855)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (862)..(867)
; OTHER INFORMATION:
US-10-651-453-16

Query Match 87.1%; Score 799.6; DB 17; Length 867;
Best Local Similarity 94.0%; Pred. No. 1.8e-237;
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;
```

```
QY 1 GAATTCATGAAAAAACCCTATCGGATCGGATGGAAGTGGCTGGTTTCCTACCGTT 60
DB 1 GAATTCATGAAAAAACCCTATCGGATCGGATGGAAGTGGCTGGTTTCCTACCGTT 60
QY 61 GCGCAGCCGATATGTGTGAAGCAGTCTCCAGGACCCCTGTTGTCTCCAGGGAA 120
DB 61 GCGCAGCCGATATGTGTGAAGCAGTCTCCAGGACCCCTGTTGTCTCCAGGGAA 120
QY 121 AAGCCACCTCTCTCTGCAAGGCGAGTCAAGAGTTAGTAGAGCTTAAGCTGTGAC 180
DB 121 AAGCCACCTCTCTCTGCAAGGCGAGTCAAGAGTTAGTAGAGCTTAAGCTGTGAC 180
QY 181 CAGCAGAACTGGCCAGGCTCCAGGCTCCATCTATGTCAGTCCACACGAGGCACT 240
DB 181 CAGCAGAACTGGCCAGGCTCCAGGCTCCATCTATGTCAGTCCACACGAGGCACT 240
```



QY 661 GATCCGTAAGGGCCGATTCACCATCTCCAGAGACATTCGAAGAACGGGTATCTA 720  
|  
|  
|  
Db 258 GATCGGTGAAGGGCCGATTCACCATCTCCAGAGACATTCGAAGAACGGGTATCTA 139  
|  
|  
|  
QY 721 AAAATGAACGCTTGAACTGAGACACGGCTGTCTATTACTGTGCGAGATCAGAC 780  
|  
|  
|  
Db 198 AAAATGAACGCTTGAACTGAGACACGGCTGTCTATTACTGTGCGAGATCAGAC 139  
|  
|  
|  
QY 781 CTGTTGGGTGATATACCACTACTAGTTTGGAGTCTGGGGCAAGGACCAAGTTC 840  
|  
|  
|  
Db 138 CTGTTGGGTGATATACCACTACTAGTTTGGAGTCTGGGGCAAGGACCAAGTTC 79  
|  
|  
|  
QY 841 ACCGTCTCTCAGATCCGAAACAAATGATCAGGGAAGAAATCTGAACCATCAGT 900  
|  
|  
|  
Db 78 ACCGTCTCTCAGATCCGAAACAAATGATCAGGGAAGAAATCTGAACCATCAGT 19  
|  
|  
|  
QY 901 CACCATTAAGTGAAGCTT 918  
|  
|  
|  
Db 18 CACCATTAAGTGAAGCTT 1

RESULT 8  
US-10-453-18/c  
; Sequence 18, Application US/10651453  
; Publication No. US20040091484A1  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; APPLICANT: Malt, Pradip K.  
; APPLICANT: Kaplan, Howard A.  
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS.  
; TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PRO  
; FILE REFERENCE: 316082000103  
; CURRENT APPLICATION NUMBER: US/10/651,453  
; PRIOR FILING DATE: 2003-08-29  
; PRIOR APPLICATION NUMBER: US 09/782,397  
; PRIOR FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: US 08/862,124  
; PRIOR FILING DATE: 1997-05-22  
; PRIOR APPLICATION NUMBER: US 08/657,449  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 867  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-10-651-453-18

Query Match 86.9%; Score 798; DB 17; Length 867;  
Best Local Similarity 93.9%; Pred. No. 5,6e-237;  
Matches 862; Conservative 0; Mismatches 5; Indels 51; Gaps 1;  
QY 1 GAATTCATGAATAAAACCGCTATCGGATCGAGTTGCTGGCTGGTTCCTACCGTT 60  
|  
|  
|  
Db 867 GAATTCATGAATAAAACCGCTATCGGATCGAGTTGCTGGCTGGTTCCTACCGTT 808  
|  
|  
|  
QY 61 GCGCAGCGCGATATGTGTGAGAGCAGTCTCCAGAGCACTCTTGTCTCCAGGGGAA 120  
|  
|  
|  
Db 807 GCGCAGCGCGATATGTGTGAGAGCAGTCTCCAGAGCACTCTTGTCTCTCAAGGGAA 748  
|  
|  
|  
QY 121 AGAGCCACCTCTCTCTGAGGGCCAGTCAGAGTTAGTAGAGCTACTTACCTGGTAC 180  
|  
|  
|  
Db 747 AGAGCCACCTCTCTCTGAGGGCCAGTCAGAGTTAGTAGAGCTACTTACCTGGTAC 688  
|  
|  
|  
QY 181 CAGCAGAACTGCGCAGGCTCCAGGCTCCATCTATAGTGGTCCAGCAGGCGCACT 240  
|  
|  
|  
Db 687 CAGCAGAACTGCGCAGGCTCCAGGCTCCATCTATAGTGGTCCAGCAGGCGCACT 628  
|  
|  
|  
QY 241 GGCATGCCAGAGGTTCAAGTGGCAGTGGTCCGGGACAGACTTCACTCTACCATCACT 300  
|  
|  
|  
Db 627 GGCATGCCAGAGGTTCAAGTGGCAGTGGTCCGGGACAGACTTCACTCTACCATCACT 568

QY 301 AGACTGAGCCCTGAAGATTTTTCAGTATTACTGTGACAGATATGATGATCACTCAG 360  
|  
|  
|  
Db 567 AGACTGAGCCCTGAAGATTTTTCAGTATTACTGTGACAGATATGATGATCACTCAG 508  
|  
|  
|  
QY 361 ACACCTCAGATCACTTTCGCGAGGAGCAAGGTGAGATCAAGAACTGTGCTGCA 420  
|  
|  
|  
Db 507 ACACCTCAGATCACTTTCGCGAGGAGCAAGGTGAGATCAAGAACTGTGCTGCA 448  
|  
|  
|  
QY 421 CCATCTGTCTGCGCGGTCCGTTCCGAGGTGTGATCAAGTGAAGTGTCTCCAG 480  
|  
|  
|  
Db 447 TC-----CGACAG 439  
|  
|  
|  
QY 481 GTCAGCTGTGAGATCTGGGGAGGCGTGTCCAGCTGGAGGCTCCAGACTCTCC 540  
|  
|  
|  
Db 438 GTCAGCTGTGAGATCTGGGGAGGCGTGTCCAGCTGGAGGCTCCAGACTCTCC 379  
|  
|  
|  
QY 541 TGTGAGCTCTGTGATTTCCCTTCAGAACTTTGTCTATGCTAGTGTCCGAGGCTCTA 600  
|  
|  
|  
Db 378 TGTGAGCTCTGTGATTTCCCTTCAGAACTTTGTCTATGCTAGTGTCCGAGGCTCTA 319  
|  
|  
|  
QY 601 GCGAAGGGCTGAGAGTGGTGGCAGTTATATATATGATGAGACCTAAATATACGCA 660  
|  
|  
|  
Db 318 GCGAAGGGCTGAGAGTGGTGGCAGTTATATATATGATGAGACCTAAATATACGCA 259  
|  
|  
|  
QY 661 GATCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTCGAAGAACGGGTATCTA 720  
|  
|  
|  
Db 258 GATCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTCGAAGAACGGGTATCTA 199  
|  
|  
|  
QY 721 AAAATGAACGCTTGAACTGAGACACGGCTGTCTATTACTGTGCGAGATCAGAC 780  
|  
|  
|  
Db 198 AAAATGAACGCTTGAACTGAGACACGGCTGTCTATTACTGTGCGAGATCAGAC 139  
|  
|  
|  
QY 781 CTGTTGGGTGATATACCACTACTAGTTTGGAGTCTGGGGCAAGGACCAAGTTC 840  
|  
|  
|  
Db 138 CTGTTGGGTGATATACCACTACTAGTTTGGAGTCTGGGGCAAGGACCAAGTTC 79  
|  
|  
|  
QY 841 ACCGTCTCTCAGATCCGAAACAAATGATCAGGGAAGAAATCTGAACCATCAGT 900  
|  
|  
|  
Db 78 ACCGTCTCTCAGATCCGAAACAAATGATCAGGGAAGAAATCTGAACCATCAGT 19  
|  
|  
|  
QY 901 CACCATTAAGTGAAGCTT 918  
|  
|  
|  
Db 18 CACCATTAAGTGAAGCTT 1

RESULT 9  
US-10-409-938-20  
; Sequence 20, Application US/10409938  
; Publication No. US2003021973A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark et al.  
; TITLE OF INVENTION: ANTIBODY GENE TRANSFER AND RECOMBINANT AAV THEREFOR  
; FILE REFERENCE: 28335/39282  
; CURRENT APPLICATION NUMBER: US/10/409,938  
; PRIOR FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: US 60/371,501  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 840  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(840)  
; OTHER INFORMATION:  
US-10-409-938-20

Query Match 43.1%; Score 395.2; DB 17; Length 840;  
Best Local Similarity 72.1%; Pred. No. 6.1e-112;  
Matches 590; Conservative 0; Mismatches 183; Indels 45; Gaps 4;

QY 56 CCGTTCGCGAGGCCATATTGTGTGACGCAAGTCCAGCAACCCGTGTTGTCTCCAG 115  
DB 50 CCAATGGTGGGCGCATATTGTGTGACGCAAGTCCAGCAACCCGTGTTGTCTCCAG 109  
QY 116 GGGAAAGAGCCACCCCTCTCTGCGAGGGCAGTCAAGATGTAGTACACTTAAGCCT 175  
DB 110 GGGAAAGAGCCACCCCTCTCTGCGAGGGCAGTCAAGATGTAGTACAGGGCTCTTAAGCCT 169  
QY 176 GGTACAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGTGATCCAGAGG 235  
DB 170 GGTACAGCAGAAACCTGCTGAGGCTCCAGGCTCTCATCTATGTGTGATCCAGAGG 229  
QY 236 CCACTGGCATGCGACAGGTCAGTGGAGGAGTGGGTCGGGACAGACTTCACTTCACCA 295  
DB 230 CCACTGGCATGCGACAGGTCAGTGGAGGAGTGGGTCGGGACAGACTTCACTTCACCA 289  
QY 296 TCAGTAGCTGAGGCTGGAAGATTTTGCAGTGTATTACTGTGACAGATATGTAGCTCAC 355  
DB 290 TCGGCGAGTGTGAGCCTGGAAGATCTGCGAGTATATTACTGTGACAGATATGTAGCTCAC 349  
QY 356 CTCAGACACCTCATGATCACTTTTCGCGAGGACCAAGGTGAGATCAACGAACTGTGG 415  
DB 350 C-----GTACACTTTTGGCCAGGCGGACCAAGTGGATCAAACTGTGTGGCG 397  
QY 416 CTGCAACATCTGTCTGTGGCGGTGGGCTTCGAGAGTGTGATGAGGTGAGGCGCT 475  
DB 398 -----GTGCTCGGCGGCGGTTCAGGTGCGGTGCTC-----TAGATCTT 442  
QY 476 CCCAGGTGAGCTGTGAGATCTGCGAGGAGCCTGTGTCAGCCTGGAAGTCCCTGAGAC 535  
DB 443 CCCAGGTGAGCTGTGAGATCTGCGAGGAGTGTGAGGAGGAGTGTGAGTCTGCTGCTGAG 502  
QY 536 TCTCTGTGCAAGCTCTGTGATTTCCCTTCAAGACTTTGCTATGACTGTGGTCCGCAAG 595  
DB 503 TCTCTGTGCAAGGCTCTGTGAGGAGCCTTCAAGATGTATGTGTTCAACTGTGGTCCGCAAG 562  
QY 596 CTCTAGGCAAGGGGCTGAGTGGGTGGGAGTTATCATATGATGAGACACTAAATTACT 655  
DB 563 CCCCTGGAATGCTCTGTGAGTGTGAGGAGTCAATCCCTATCTTTGTGACTCAACT 622  
QY 656 AGCAGACTCCCTGAGAGGCGGATTCACATCTCCAGAGACACTTCCAGAAACACGGTGT 715  
DB 623 AGCAGAGAGTTCGCGGGGAGAGTCAAGTTTACCGGGACCAAGCAGAGACAGCCT 682  
QY 716 ATCTAAAAATGAACAGCTGTGAGAACTGAGAGACAGGCTGTCTATTTACTGTGCGAGATC 775  
DB 683 ACATGAGGTGACCAACTGCGATCTGACGACAGCAGGCGGTCTATTTATGTGCGAGAGAT 742  
QY 776 AGAGCTGTGGGTGACTATGACCACTACAGGT-----TTGAGAG 817  
DB 743 TTGGCCCCGAGTGGAAAGACGTGATTCCTATGATGTAGTGGCCGGGGTCTTTGACT 802  
QY 818 TCTGGGCAAGAGGACCAAGCTCACCGTCTCTCAAGA 855  
DB 803 TCTGGGGCCAGGAGACCTGTGTCAAGCTCTCTCAAGA 840

RESULT 10  
US-09-782-397-6/c  
; Sequence 6, Application US/09782397  
; Publication No. US2003002179A1  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; Maitl, Pradip K.  
; Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Morrison & Foerster LLP  
STREET: 755 Page Mill Road

CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 450 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-782-397-6  
Query Match 39.3%; Score 361; DB 10; Length 450;  
Best Local Similarity 100.0%; Pred. No. 2.1e-101; Indels 0; Gaps 0;  
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 70 GATATTGTGTGAGCAGCTCCAGGACCCGTCTTTGTCTCCAGGGAAAGACCAACC 129  
DB 378 GATATTGTGTGAGCAGCTCCAGGACCCGTCTTTGTCTCCAGGGAAAGACCAACC 319  
QY 130 CTCTCCTGAGGCGCAGTCAAGATGTAGTACAGCTTAAGCTGTGATCCAGAGAAA 189  
DB 318 CTCTCCTGAGGCGCAGTCAAGATGTAGTACAGCTTAAGCTGTGATCCAGAGAAA 259  
QY 190 CTTGGCAGGCTCCAGGCTCTCATCTATGTGTGATCCAGAGGCGCATGGCA 249  
DB 258 CTTGGCAGGCTCCAGGCTCTCATCTATGTGTGATCCAGAGGCGCATGGCA 199  
QY 250 GACAGGTCAAGTGGAGTGGGTCCGGGACAGACTTCACTTCACCATGATGAGCTGAG 309  
DB 198 GACAGGTCAAGTGGAGTGGGTCCGGGACAGACTTCACTTCACCATGATGAGCTGAG 139  
QY 310 CTTGAAGATTTTGCAGTGTATTACTGTGACAGATATGTAGTCACTTCAGACCTCAG 369  
DB 138 CTTGAAGATTTTGCAGTGTATTACTGTGACAGATATGTAGTCACTTCAGACCTCAG 79  
QY 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAAGAACTGTGGCTGCAACATCTGTC 429  
DB 78 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAAGAACTGTGGCTGCAACATCTGTC 19  
QY 430 T 430  
DB 18 T 18

RESULT 11  
US-10-651-453-6/c  
; Sequence 6, Application US/10651453  
; Publication No. US20040091484A1  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; Maitl, Pradip K.

```
/ APPLICANT: Kaplan, Howard A.
/ TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS,
/ NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PRO
/ TITLE OF INVENTION: DETECTION OF CANCERS
/ FILE REFERENCE: 316082000103
/ CURRENT APPLICATION NUMBER: US/10/651,453
/ CURRENT FILING DATE: 2003-08-29
/ PRIOR APPLICATION NUMBER: US 09/782,397
/ PRIOR FILING DATE: 2001-02-13
/ PRIOR APPLICATION NUMBER: US 08/862,124
/ PRIOR FILING DATE: 1997-05-22
/ PRIOR APPLICATION NUMBER: US 08/657,449
/ PRIOR FILING DATE: 1996-05-22
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 6
/ LENGTH: 450
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
US-10-651-453-6

Query Match          39.3%; Score 361; DB 17; Length 450;
Best Local Similarity 100.0%; Pred. No. 2,1e-101;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 GATATTGTGTGACGAGCTCTCCAGGCACTCTTTGTCTCCAGGGGAAAAGGCCACC 129
DB |||||||
DB 378 GATATTGTGTGACGAGCTCTCCAGGCACTCTTTGTCTCCAGGGGAAAAGGCCACC 319
QY 130 CTCTCTGAGGGGCGAGAGGTGTTAGAGAGTACTTACCGTGGTACAGAGAGAA 189
DB |||||||
DB 318 CTCTCTGAGGGGCGAGAGGTGTTAGAGAGTACTTACCGTGGTACAGAGAGAA 259
QY 190 CTGGCCAGGCTCCAGGCTCTCTCATCTATGTGTGATCCAGGAGGCACTGGATGCCA 249
DB 258 CTGGCCAGGCTCCAGGCTCTCTCATCTATGTGTGATCCAGGAGGCACTGGATGCCA 199
QY 250 GACAGGTTAGTGGCAGTGGGTCCGGGACAGACTTCACTCTCACTCATCATGATCTGGAG 309
DB 198 GACAGGTTAGTGGCAGTGGGTCCGGGACAGACTTCACTCTCACTCATCATGATCTGGAG 139
QY 310 CCTGAAGATTTTGGCAGTGTATTACTGTGACAGATAGTGAAGCTTCACTGACACTCTGAG 369
DB 138 CCTGAAGATTTTGGCAGTGTATTACTGTGACAGATAGTGAAGCTTCACTGACACTCTGAG 79
QY 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAAGAACTGTGGCTGACCATCTGTTC 429
DB 78 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAAGAACTGTGGCTGACCATCTGTTC 19
QY 430 T 430
DB 18 T 18

RESULT 12
US-09-782-397-4
/ Sequence 4, Application US/09782397
/ Publication No. US20030021779A1
/ GENERAL INFORMATION:
/ APPLICANT: Dan, Michael D.
/ Mailei, Pradip K.
/ KAPLAN, Howard A.
/ TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
/ SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
/ FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
/ DETECTION OF CANCERS
/ NUMBER OF SEQUENCES: 28
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Morrison & Foerster LLP
/ STREET: 755 Page Mill Road
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
```

```
ZIP: 94304-1018
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/782,397
/ FILING DATE: 13-Feb-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/862,124
/ FILING DATE: 1997-05-22
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lehnhardt, Susan K.
/ REGISTRATION NUMBER: 33,943
/ REFERENCE/DOCKET NUMBER: 31608-20001.20
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 813-5600
/ TELEFAX: (650) 494-0792
/
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 450 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..450
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-782-397-4

Query Match          39.2%; Score 359.4; DB 10; Length 450;
Best Local Similarity 99.7%; Pred. No. 6.5e-101;
Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 70 GATATTGTGTGACGAGCTCTCCAGGCACTCTTTGTGTCTCCAGGGGAAAAGGCCACC 129
DB |||||||
DB 73 GATATTGTGTGACGAGCTCTCCAGGCACTCTTTGTGTCTCCAGGGGAAAAGGCCACC 132
QY 130 CTCTCTGAGGGGCGAGAGGTGTTAGAGAGTACTTACCGTGGTACAGAGAGAA 189
DB |||||||
DB 133 CTCTCTGAGGGGCGAGAGGTGTTAGAGAGTACTTACCGTGGTACAGAGAGAA 192
QY 190 CTGGCCAGGCTCCAGGCTCTCTCATCTATGTGTGATCCAGGAGGCACTGGATGCCA 249
DB 193 CTGGCCAGGCTCCAGGCTCTCTCATCTATGTGTGATCCAGGAGGCACTGGATGCCA 252
QY 250 GACAGGTTAGTGGCAGTGGGTCCGGGACAGACTTCACTCTCACTCATCATGATCTGGAG 309
DB 253 GACAGGTTAGTGGCAGTGGGTCCGGGACAGACTTCACTCTCACTCATCATGATCTGGAG 312
QY 310 CCTGAAGATTTTGGCAGTGTATTACTGTGACAGATAGTGAAGCTTCACTGACACTCTGAG 369
DB 313 CCTGAAGATTTTGGCAGTGTATTACTGTGACAGATAGTGAAGCTTCACTGACACTCTGAG 372
QY 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAAGAACTGTGGCTGACCATCTGTTC 429
DB 373 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAAGAACTGTGGCTGACCATCTGTTC 432
QY 430 T 430
DB 433 T 433

RESULT 13
US-10-651-453-4
/ Sequence 4, Application US/10651453
/ Publication No. US20040091484A1
/ GENERAL INFORMATION:
/ APPLICANT: Dan, Michael D.
/ Mailei, Pradip K.
```

```
/ APPLICANT: Kaplan, Howard A.
/ TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS,
/ TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PRO
/ TITLE OF INVENTION: DETECTION OF CANCERS
/ FILE REFERENCE: 31608200103
/ CURRENT APPLICATION NUMBER: US/10/651,453
/ PRIOR FILING DATE: 2003-08-29
/ PRIOR APPLICATION NUMBER: US 09/782,397
/ PRIOR FILING DATE: 2001-02-13
/ PRIOR APPLICATION NUMBER: US 08/862,124
/ PRIOR FILING DATE: 1997-05-22
/ PRIOR APPLICATION NUMBER: US 08/657,449
/ PRIOR FILING DATE: 1996-05-22
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 450
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
US-10-651-453-4

Query Match          39.2%; Score 359.4; DB 17; Length 450;
Best Local Similarity 99.7%; Pred. No. 6.5e-101;
Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 70 GATATTGTTGACGAGCTCTCCAGGACCCCTGTTCTTTGTTCTTCAGGGGAAAGGCCACC 129
DB 73 GATATTGTTGACGAGCTCTCCAGGACCCCTGTTCTTTGTTCTTCAGGGGAAAGGCCACC 132
QY 130 CTCTCTGAGGGCCAGTACAGAGTGTAGTACAGCTACTAGCCGTGTACAGAGAAA 189
DB 133 CTCTCTGAGGGCCAGTACAGAGTGTAGTACAGCTACTAGCCGTGTGTACAGAGAAA 192
QY 190 CCTGGCCAGGCTCCAGGCTCTCATCTATGTGTGATCCACAGGGCCACTGGCATGCCA 249
DB 193 CCGGCGCAGGCTCCAGGCTCTCATCTATGTGTGATCCACAGGGCCACTGGCATGCCA 252
QY 250 GACAGGTTGAGTGGCAGTGGGTCCGGACAGATCTTCACTCCATCACTAGTACGTGGAG 309
DB 253 GACAGGTTGAGTGGCAGTGGGTCCGGACAGATCTTCACTCCATCACTAGTACGTGGAG 312
QY 310 CCTGAAGATTTTGCAGTGTATTACTGTACAGCAGTATGTAGTACCTCAGACCTCAG 369
DB 313 CCTGAAGATTTTGCAGTGTATTACTGTACAGCAGTATGTAGTACCTCAGACCTCAG 372
QY 370 ATCACTTTGCGCGAGAGCAACAAGTGAAGATCAAAAGACTGTGGCTGACCATCTGTC 429
DB 373 ATCACTTTGCGCGAGAGCAACAAGTGAAGATCAAAAGACTGTGGCTGACCATCTGTC 432
QY 430 T 430
DB 433 T 433

RESULT 14
US-10-423-847-8
/ Sequence 8, Application US/10423847
/ Publication No. US2004009166A1
/ GENERAL INFORMATION:
/ APPLICANT: FILIPULA, DAVID RAY
/ APPLICANT: BASU, KAREN
/ APPLICANT: BASU, AMARITA
/ APPLICANT: WANG, MAOLING
/ TITLE OF INVENTION: SINGLE CHAIN ANTIGEN-BINDING POLYPEPTIDES FOR POLYMER
/ TITLE OF INVENTION: CONJUGATION
/ FILE REFERENCE: 213,1180
/ CURRENT APPLICATION NUMBER: US/10/423,847
/ CURRENT FILING DATE: 2003-04-25
/ PRIOR APPLICATION NUMBER: 09/791,578
/ PRIOR FILING DATE: 2001-02-26
/ PRIOR APPLICATION NUMBER: 09/791,540
/ PRIOR FILING DATE: 2001-02-26
/ PRIOR APPLICATION NUMBER: 09/069,842
```

```
/ PRIOR FILING DATE: 1998-04-30
/ PRIOR APPLICATION NUMBER: 60/044,449
/ PRIOR FILING DATE: 1997-04-30
/ PRIOR APPLICATION NUMBER: 60/050,472
/ PRIOR FILING DATE: 1997-06-23
/ PRIOR APPLICATION NUMBER: 60/063,074
/ PRIOR FILING DATE: 1997-10-27
/ PRIOR APPLICATION NUMBER: 60/067,341
/ PRIOR FILING DATE: 1997-12-02
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 762
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(762)
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic 2-7-SC-8
US-10-423-847-8

Query Match          36.8%; Score 337.8; DB 17; Length 762;
Best Local Similarity 69.1%; Pred. No. 3.9e-94;
Matches 541; Conservative 0; Mismatches 197; Indels 45; Gaps 4;

QY 69 GATATTGTTGTTGACGAGCTCTCCAGGACCCCTGTTCTTTGTTCTTCAGGGGAAAGGCCAC 128
DB 3 CACATCTCAAGATGAGCCAGTCTCCATCTCTCTGTTCTGATCTGTAGGGGACAGAGTAC 62
QY 129 CCTTCCGAGGGCCAGTACAGAGTGTAGTACAGCTACTAGCCGTGTACAGAGAAA 188
DB 63 CATCTGTTGCGGAGAGTCAAG--GCACTCAAGAAATTACTTAGCTGGTATCAAGCAAAA 119
QY 189 ACCTGGCCAGGCTCCAGGCTCTCATCTATGTGTGATCCACAGGGCCACTGGCATGCC 248
DB 120 ACCAGGAAAGCCCTTAGTCTCTGATCTATGCTGATCTGATCTGATCTGATCTGATCTG 179
QY 249 AGACAGGTTGAGTGGCAGTGGGTCCGGACAGATCTTCACTCCATCACTAGTACGTGGAG 308
DB 180 ATCTGGTTCAGTGGCAGTGGGTCCGGACAGATCTTCACTCCATCACTAGTACGTGGAG 239
QY 309 GCTGAAGATTTTGCAGTGTATTACTGTACAGCAGTATGTAGTACCTCAGACCTCAG 368
DB 240 GCTGAAGATTTTGCAGTGTATTACTGTACAGCAGTATGTAGTACCTCAGACCTCAG 287
QY 369 GATCACTTTGCGCGAGAGCAACAAGTGAAGATCAAAAGACTGTGGCTGACCATCTGTC 428
DB 288 GATATCTTTGCGCGAGAGCAACAAGTGAAGATCAAAAGACTGTGGCTGACCATCTGTC 330
QY 429 CTCTGGCGGTGCGGCTTCCGAGGTGTGTGATCAAGTGAAGTGTGCTCCAGAGTGAAGCT 488
DB 331 -ACTAGTGTAGTGGCGCAAACTCCGAGAGTGTGTGATCAAGTGAAGTGTGAGTGAAGCT 389
QY 489 GGTGAAGTGTGGGGAGAGGTGTGATCAAGTGAAGTGTGATCAAGTGAAGTGTGATCAAGT 548
DB 390 GGTGAAGTGTGGGGAGAGGTGTGATCAAGTGAAGTGTGATCAAGTGAAGTGTGATCAAGT 449
QY 549 CTCTGATTTCCCTTCAGAACTTTGCTATGATCACTGGGTCCGCAAGCTCTTAGGCAAGGG 608
DB 450 CTCTGATTTCACTTTGATGATTTATGATGATGATGATGATGATGATGATGATGATGATG 509
QY 609 GCTGAAGTGTGGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 668
DB 510 CCGTAATGGGTCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 569
QY 669 GAAAGGCCATTTCACTATCTCAAGAGCACTTCAAGAGCAAGGTGTATCTAATAATGAA 728
DB 570 GGAAGGCCATTTCACTATCTCAAGAGCAAGGTGTATCTAATAATGAA 629
QY 729 CAGCTGAAGACTGAGAGCACGAGTGTATTAATGATGATGATGATGATGATGATGATGATGAT 788
```





**THIS PAGE BLANK (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 18, 2005, 08:24:33 ; Search time 25 Seconds

(without alignments)  
7066.159 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 1713  
Sequence: 1 GAATTCATGAAAAAACCGC.....ATCACATTATGTAAGCTT 918

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+n2p.model -DEV=xlh  
-Q=/cgn2.1/USPTO.spool/US09194164/runat.16022005.122613.6034/app.query.fasta\_1.1095  
-DB=PIR\_7g -QFMT=fastan -SUFFIX=xpr -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human0.cdf -LIST=45  
-LOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09194164@cgn.1.1.26@runat.16022005.122613.6034 -NCPU=6 -ICPU=3  
-NO.WMAP -LARGESUBJECT -NEG.SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR\_7g:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541.5	31.6	122	2	E36005 Ig heavy chain V r
2	539.5	31.5	128	2	S48797 Ig heavy chain V r
3	537.5	31.4	215	2	A23746 Ig kappa chain V-I
4	534	31.2	109	2	G30607 Ig kappa chain V-I
5	531	31.0	122	2	S31119 Ig heavy chain - h
6	530	30.9	109	2	A30608 Ig kappa chain V-I
7	530	30.9	109	2	B30601 Ig kappa chain V-I
8	529	30.9	109	2	D30601 Ig kappa chain V-I
9	528.5	30.9	108	2	H44151 Ig kappa chain V r
10	527.5	30.8	215	2	JB0242 Ig kappa chain V r
11	527	30.8	109	2	C30601 Ig kappa chain V-I
12	526	30.7	109	2	F30607 Ig kappa chain V-I
13	526	30.7	129	1	K3H04 Ig kappa chain pre
14	525	30.6	123	2	S38493 Ig heavy chain - h

15	525	30.6	129	2	S49532 anti-Sm antibody V
16	524	30.6	109	2	H30601 Ig kappa chain V-I
17	523	30.5	109	1	K3H051 Ig kappa chain V-I
18	522.5	30.5	114	2	S46375 Ig kappa chain V-J
19	522	30.5	109	2	PH0963 Ig kappa chain V r
20	521	30.4	109	2	G30601 Ig kappa chain V-I
21	520	30.4	129	1	K3H04 Ig kappa chain pre
22	518	30.2	108	2	C30608 Ig kappa chain V-I
23	516	30.1	129	2	S46369 Ig kappa chain var
24	516	30.1	134	2	S38643 Ig kappa chain V r
25	515	30.1	107	2	PH0965 Ig kappa chain V r
26	514	30.0	108	2	B30608 Ig kappa chain V-I
27	514	30.0	145	2	S20631 Ig kappa chain - h
28	513	29.9	119	2	F36005 Ig heavy chain V r
29	512	29.9	109	2	F30601 Ig kappa chain V-I
30	510.5	29.8	104	2	PH0964 Ig kappa chain V r
31	510	29.8	109	1	K3H051 Ig kappa chain V-I
32	510	29.8	128	2	S20636 Ig kappa chain V r
33	509	29.7	121	2	G36005 Ig heavy chain V r
34	508	29.7	134	2	S31679 Ig heavy chain V r
35	507.5	29.6	110	2	E30607 Ig kappa chain V-I
36	507.5	29.6	114	2	S46390 Ig heavy chain V r
37	507.5	29.6	147	2	I37780 Ig variable region
38	506	29.5	109	1	K3H04 Ig kappa chain V-I
39	505	29.5	109	2	F44151 Ig kappa chain V r
40	504.5	29.5	122	2	S31117 Ig heavy chain - h
41	504	29.4	132	2	S31603 Ig heavy chain V r
42	503.5	29.4	108	2	E30609 Ig kappa chain V-I
43	503	29.4	130	2	PL0098 Ig heavy chain pre
44	503	29.4	133	2	A49028 Ig heavy chain V-I
45	502.5	29.3	110	2	S44120 Ig kappa chain V-J

#### ALIGNMENTS

RESULT 1  
E36005  
Ig heavy chain V region (M72) - human  
C/Dates: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Dec-1998  
C/Accession: E36005  
R/Schroeder Jr., H.W.; Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
A/Reference number: A36005; MUID:90349571; PMID:2117273  
A/Accession: E36005  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-122 <SCH>  
A/Cross-References: GB:M34030  
C/Genetics:  
A/Gene: GDB:IGH@; IGHDX1  
A/Cross-References: GDB:118731; OMIM:146910  
A/Map position: 14q32.33-14q32.33  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-98/Domain: immunoglobulin homology <1M>

#### Alignment Scores:

Pred. No.: 6,876-31  
Score: 541.50  
Percent Similarity: 88.80%  
Best Local Similarity: 84.00%  
Query Match: 31.61%  
DB: 2  
Gaps: 1

US-09-194-164-13 (1-918) x E36005 (1-122)

QY 478 CAGGTGACGCTGGTGGAGCTTGGGGAGCCGTGTCACGCTGGAGAGTCCCTGAGACTC 537  
DB 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20  
QY 538 TCTGTGACGCTCTGAGATTCCCTTCAGAAAGCTTGTGTAAGCACTGGGTCCGCAAGCT 597

Db	21	SerCysAlaIalaSerGlyPheThrPheSerSerTyrAlaMetHisTrpValArgGlnAla	40
Qy	598	CTAGGCAAGGGGCGTGGAGTGGGTGGCGATTATATCATATGATGAGACCTAAATACTAC	657
Db	41	ProdiLysGlyLeuGlnIuTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyr	60
Qy	658	GCACACTCCGTGAAGGGCCGATTACACANTCTCAGAGACACTTCCAGAAACAGGTGAT	717
Db	61	AlaAspSerValLysGlyIaTrpPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr	80
Qy	718	CTAAATAATGAACGCTGAGAACTGAGACACAGCGTGTCTATTACTGTGGCAGAGATCAG	777
Db	81	LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArgAspArg	100
Qy	778	AGCCTGTGGGTGATCATATGACCACTATCAACGGTTTGGACGCTCGGGGCAAGGGACACG	837
Db	101	His-----SerSerSerTrpTyrTyrGlyMetAspValTrpGlyGlnGlyThrThr	117
Qy	838	GTACACGCTCTCTCA	852
Db	118	ValThrValSerSer	122

## RESULT 2

Ig heavy chain V region (anti-5m, VH3/Dxp4/JH6) - human (fragment)  
CSpecies: Homo sapiens (man)  
CDate: 13-Jan-1995 #sequence\_revision 13-Sep-1998 #text\_change 23-Jul-1999  
CAccession: S48797, S26893  
R:Mamoudi, M.; Edwards, J.; Cairne, E.; Bell, D.  
submitted to the EMBL Data Library, October 1994  
A:Description: Molecular characterization of natural human anti-5m autoantibodies.  
A:Reference number: S48797  
A:Accession: S48797  
A:Molecule type: mRNA  
A:Residues: 1-128 <MA>  
A:Cross-references: EMBL:Z46379, NID:g587147, PIDN:CAA66512.1, PID:g1340168  
R:TOMLINSON, I.M.; Walter, G.; Marks, J.D.; Dlewelyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
A:Reference number: S26885, MUID:9302117, PMID:1404388  
A:Accession: S26893  
A:Molecule type: DNA  
A:Residues: 1-98 <TM>  
A:Cross-references: EMBL:Z12350, NID:g32922, PIDN:CAA76220.1, PID:g329223  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
P:15-98/Domain: immunoglobulin homology <IM>

### Alignment Scores:

Pred. No.:	9.51e-31	Length:	128
Score:	539.50	Matches:	105
Percent Similarity:	86.72%	Conservative:	6
Best Local Similarity:	82.03%	Mismatches:	14
Query Match:	31.49%	Indels:	
DB:	2	Gaps:	1

US-09-194-164-13 (1-918) X S48797 (1-128)

QY 478 CAGGTGACAGCTGGTGGAGAGTCTGGGGAGGCGGTGCTCCAGCTCGGAAGTCCCTGAACTC 537

Db 1 GlnValGlnLeuValGlnSerGlyGlyGlyValValGlnProGlyArgSerLeuArgLeu 20

QY 538 TCCGTGCGACCTCTGAGATTCCCTTCAAGACTTGGTATGACACTGGGTCCGCAAGCT 597

Db 21 SerCysAlaIaSerGlyPheThrPheSerSerTyrglyMetHisThrValArgGlnAla 40

QY 598 CTAGCGAAGGGGCTGGAGTGGGTGGCGAGTATATATATATATGATGAAGACATTAATATAC 657

Db 41 ProGlyIysGlyLeuGlnIleuTrpValAlaValIleTrpIleArgIleSerAlaIysSerAlaIysTygTyr 60

QY 658 GCAGATCCGTGAAGGGCCGATTACACATCTCCAAAGACACTTCCAAAGAACGGGTAT 717

Db	61	AlaAspSerValLysIleYrPherThrIleSerArgAspAsnSerIysAsnThrLeuTyr	80
Qy	718	CTAAAAATGAACGCTGTGAACCTAGAGACACGCGTGTCTTATTAAGTGTGGACGAGATCAG	777
Db	81	LeuGlnMetAsnSerLeuArgIleGluAspThrIleValTyrTyrCysAlaArgAspAsn	100
Qy	778	-----AGCCTGTTGGGTGACATATGACCACTACTACGCTTTGGACGCTCGGGCGAA	828
Db	101	TyrTyrTyrAspSerSerIleTyrTyrTyrTyrTyrTyrTyrGlyMetAspValThrGlyGln	120
Qy	829	GGAGACACGCGTCAACGCTCCCTCA	852
Db	121	GlyThrThrValThrValSerSer	128

### RESULT 3

Ig kappa chain V-II (Kb) cold agglutinin) - human  
C:Species: Homo sapiens (man)  
C:date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
C:Accession: A23746  
R:Leonl, J.; Ghiso, J.; Goni, F.; Frangione, B.  
J Biol Chem. 266, 2836-2842, 1991  
A:Title: The primary structure of the Fab fragment of protein Kb, a monoclonal immunoglobulin  
A:Reference number: A23746; MIMD:91131575; PMID:1993660  
A:Accession: A23746  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-215 <LEO>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

**Alignment Scores:**

Pred. No.:	1,3e-30	length:	125
Score:	537.50	Matches:	13
Percent Similarity:	64.68%	Conservative:	12
Best Local Similarity:	58.72%	Mismatches:	27
Query Match:	31.38%	Indels:	50
DB:	2	Gaps:	5

US-09-194-164-13 (1-918) X A23746 (1-215)

[illegible]

QY 550 TCTGATTCCTCCCTTCAGAGCTTGTCTATGCACTGG---GTCCGCGAGGCTTACGACAG 606  
Db 138 AaaanpHeTyRProxrgLualayValGlnTPrLyValAAspAanlaLeugInser 157  
QY 607 GGGCTGAGTGGGTGGAGCTATATATCATATGATGAGAGCACTAAATACAGCAAGATCC 666  
Db 158 GtYaanserGIncluserValThrgLugInapSerLyAspSerThrTyR-----Ser 175  
QY 667 GTGAAGGCGCATTCACATCTCCAGA---GACACTTCAGAGAACGCGTGTAT 717  
Db 176 LeuserSerThrLeuThrLeuSerLyValAspTyRGlulYValHleValTyR 193

## RESULT 4

G30607  
Ig kappa chain V-III region (Kae) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 21-Jan-2000  
C:Accession: G30607  
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc  
J. Immunol. 142, 3158-3163, 1989  
A:Title: Structural and idiotypic characterization of the L chains of human Igm autoantib  
A:Reference number: A30601; MUID:89215279; PMID:2496160  
A:Accession: G30607  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-109 <GON>  
C:Superfamily: immunoglobulin V region, immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	2,35e-30	Length:	109
Percent Similarity:	534.00	Matches:	104
Best Local Similarity:	95.58%	Conservative:	4
Query Match:	32.04%	Mismatches:	1
DB:	2	Indels:	4
		Gaps:	1

US-09-194-164-13 (1-918) x G30607 (1-109)

QY 70 GATATTGTGTGACGACAGTCTCCAGACACCTGTCTTGTCTCCAGGGGAAAGACCAAC 129  
Db 1 AsplleValleuThrGlnSerProGlyThrLeuSerLeuSerProGlyValuGlnAlaThr 20  
QY 130 CTCTCTGACAGGCGCAGTCAAGTGTATGACAGCTACTTACCTGTGACAGAGAAA 189  
Db 21 LeuserCybArGAlaSerGlnSerLeuSerThrTyRLeuAlaTriPtyGlnGlnlys 40  
QY 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGTGTCATCCACAGGCGCATGGCCA 249  
Db 41 ProGlyGlnAlaProArGLeuLeuLeuTyRGlYAlaSerSerArGAlaThrGlyValPro 60  
QY 250 GACAGGTCAGTGGCAGTGGGTCCGGAGACAGCTCACCTGCACATAGTATGATGAG 309  
Db 61 AspArGpHeSerGlySerGlySerGlySerGlyThrAspHeThrLeuThrIleSerArGLeuGlu 80  
QY 310 CCTGAAGATTTTGACGTATATTACTGTACAGCATATGAGTCACTCAGACACCTCAG 369  
Db 81 ProGluAspHeAlaValTyRtyrCybGlnGlnInTyRglYSerSerPro----- 96  
QY 370 ATCACTTTCCGGCGAGGAGCAAGAGTGAATCAACAA 408  
Db 97 PheThrPheGlyGlyGlyThrTyValGlnIleLysArG 109

## RESULT 5

G31119  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C:Accession: G31119  
R:Raaphorst, F.M.; Timmers, E.; Kenner, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmat  
Eur. J. Immunol. 22, 247-251, 1992

A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A:Reference number: G31104; MUID:92111633; PMID:1730252  
A:Accession: G31119  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-122 <RAA>  
A:Cross-references: UNIPROT:Q9UWU1; EMBL:X62970  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C:Superfamily: immunoglobulin V region, immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	3,83e-30	Length:	122
Score:	531.00	Matches:	105
Percent Similarity:	88.80%	Conservative:	6
Best Local Similarity:	84.00%	Mismatches:	11
Query Match:	31.00%	Indels:	3
DB:	2	Gaps:	1

US-09-194-164-13 (1-918) x G31119 (1-122)

QY 478 CAGTGCAGCTGTGAGTCTGGGGAGGCGTGTCCAGCCTGGAGAGTCCCTGAGACTC 537  
Db 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArGSerLeuArGLeu 20  
QY 538 TCTGTGACAGCTCTGTGATTCCTCCAGAGCTTGTCTATGATGAGAGCACTAAATCTAC 597  
Db 21 SerCybAlaAlaSerGlyPheThrPheSerSerTyRGlYMeHlStrValArGlnAla 40  
QY 598 CTAGGCAAGGCGCTGAGTGGGTGGCAGTATATCATATGATGAGAGCACTAAATCTAC 657  
Db 41 ProGlyLysGlyLeuGlnTPrValAlaValIleSerTyRAspGlySerAmnTyRtyr 60  
QY 658 GCAAGCTCCGTGAAGGCGGATTCACCATCTCCAGAGCACTCCAGAGAGCGGTAT 717  
Db 61 AlaAspSerValLyGlyArGpHeThrIleSerArGAspSerLyAsnThrLeuTyR 80  
QY 718 CTAAATAATGAACAGCCTGAGAACTGAGGACAGCGGCTGTATTACTGTGCGAGATCAG 777  
Db 81 LeuGlnMetAmSerLeuArGAlaGlnAspThrAlaValTyRtyrCybAlaLysAspGly 100  
QY 778 AGCCTGTGGGTGATATGACCATCTACAGTGTGAGCTGTGGGCGAAAGGACACAG 837  
Db 101 AlaValAlaGly-Leu-----ArgThrThrValThrPheSerGlyAlaLysGlyProAr 118  
QY 838 GTACACGCTCTCCT 850  
Db 118 GSerProSerPro 122

## RESULT 6

A30608  
Ig kappa chain V-III region (Son) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: A30608  
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo  
J. Immunol. 142, 3158-3163, 1989  
A:Title: Structural and idiotypic characterization of the L chains of human Igm autoantib  
A:Reference number: A30601; MUID:89215279; PMID:2496160  
A:Accession: A30608  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-109 <GON>  
A:Cross-references: UNIPROT:Q9UW78  
C:Superfamily: immunoglobulin V region, immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	4,52e-30	Length:	109
Score:	530.00	Matches:	104
Percent Similarity:	95.58%	Conservative:	4

Best Local Similarity: 92.04% Mismatches: 1  
 Query Match: 30.94% Indels: 4  
 DB: 2 Gaps: 1

US-09-194-164-13 (1-918) x A30608 (1-109)

```

QY 70 GATATTGTTTACCGACAGCTCCAGGACCCCTGTTTGTCTCCAGGGGAAAGACCACC 129
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1 GuilleValLeuthrInserProGlyThrLeuSerLeuSerProGlyGluArgAlaThr 20

QY 130 CTCTCCGAGGCGGCGAGTGTAGAGCTTGTAGAGCTTACCTGAGCTGTACAGAGAAA 189
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 21 LeuSerCyArGAlaSerInserValSerSerSerTyLeuAlaTrpTyrgInGlnlys 40

QY 190 CCTGGCCAGGCTCCAGGCTCCTCATCTATGTGTGATCCAGGCGGCACTGGCATGCCA 249
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 41 ProGlyGlnAlaProArgLeuLeuLeuLeuTyrglyAlaSerSerArgAlaThrGlyLePro 60

QY 250 GACAGGTTACGTGGCGAGTGGGTCCGGGACAGACTTACCTCACCATCAGTACGTGAG 309
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 61 AsnArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGln 80

QY 310 CCTGAAGATTTTGACGTGATTACTGTACAGAGTATGTAGCTCACCTCAGACACTCAG 369
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 81 ProGluAspPheAlaValAlaTyrrTyrcysGlnGlnInTyrglySerSerPro----- 96

QY 370 ATCACTTTCCGCGAGGAGCAAGAGGTGAGATCAACGA 408
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 97 TyrThrPheGlyGlyGlyThrIlyValGluIleLeuArg 109
  
```

## RESULT 7

ig kappa chain V-III region (Glo) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
 C/Accession: B30601  
 R/Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo  
 J. Immunol. 142, 3158-3163, 1989  
 A>Title: Structural and idiotypic characterization of the L chains of human IgM autoanti  
 A/Reference number: A30601; PMID:89215279; PMID:2496160  
 A/Accession: B30601  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-109 <GON>  
 A/Cross-references: UNIPROT:Q9UL78  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F,16-91/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Prod. No.: 4.52e-30 Length: 109  
 Score: 530.00 Matches: 104  
 Percent Similarity: 95.58% Conservative: 4  
 Best Local Similarity: 92.04% Mismatches: 1  
 Query Match: 30.94% Indels: 4  
 DB: 2 Gaps: 1

US-09-194-164-13 (1-918) x B30601 (1-109)

```

QY 70 GATATTGTTTACCGACAGCTCCAGGACCCCTGTTTGTCTCCAGGGGAAAGACCACC 129
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1 GuilleValLeuthrInserProGlyThrLeuSerLeuSerProGlyGluArgAlaThr 20

QY 130 CTCTCCGAGGCGGCGAGTGTAGAGCTTGTAGAGCTTACCTGAGCTGTACAGAGAAA 189
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 21 LeuSerCyArGAlaSerInserValSerSerSerTyLeuAlaTrpTyrgInGlnlys 40

QY 190 CCTGGCCAGGCTCCAGGCTCCTCATCTATGTGTGATCCAGGCGGCACTGGCATGCCA 249
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 41 ProGlyGlnAlaProArgLeuLeuLeuLeuTyrglyAlaSerSerArgAlaThrGlyLePro 60

QY 250 GACAGGTTACGTGGCGAGTGGGTCCGGGACAGACTTACCTCACCATCAGTACGTGAG 309
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
  
```

```

DB 61 AspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGln 80
QY 310 CCTGAAGATTTTGACGTGATTACTGTACAGAGTATGTGATGCTTACCTCAGACACTCAG 369
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 81 ProGluAspPheAlaValAlaTyrrTyrcysGlnGlnInTyrglySerSerPro----- 96
  
```

QY 370 ATCACTTTCCGCGAGGAGCAAGGTTGAGATCAACGA 408

DB 97 LeuThrPheGlyGlnGlyThrIlyValGluIleLeuArg 109

## RESULT 8

ig kappa chain V-III region (Cur) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
 C/Accession: D30601  
 R/Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo  
 J. Immunol. 142, 3158-3163, 1989  
 A>Title: Structural and idiotypic characterization of the L chains of human IgM autoanti  
 A/Reference number: A30601; PMID:89215279; PMID:2496160  
 A/Accession: D30601  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-109 <GON>  
 A/Cross-references: UNIPROT:Q9UL78  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F,16-91/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Prod. No.: 5.32e-30 Length: 109  
 Score: 529.00 Matches: 104  
 Percent Similarity: 95.58% Conservative: 4  
 Best Local Similarity: 92.04% Mismatches: 1  
 Query Match: 30.88% Indels: 4  
 DB: 2 Gaps: 1

US-09-194-164-13 (1-918) x D30601 (1-109)

```

QY 70 GATATTGTTTACCGACAGCTCCAGGACCCCTGTTTGTCTCCAGGGGAAAGACCACC 129
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1 GuilleValLeuthrInserProGlyThrLeuSerLeuSerProGlyGluArgAlaThr 20

QY 130 CTCTCCGAGGCGGCGAGTGTAGAGCTTGTAGAGCTTACCTGAGCTGTACAGAGAAA 189
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 21 LeuSerCyArGAlaSerInserValSerSerSerTyLeuAlaTrpTyrgInGlnlys 40

QY 190 CCTGGCCAGGCTCCAGGCTCCTCATCTATGTGTGATCCAGGCGGCACTGGCATGCCA 249
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 41 ProGlyGlnAlaProArgLeuLeuLeuLeuTyrglyAlaSerSerArgAlaThrGlyLePro 60

QY 250 GACAGGTTACGTGGCGAGTGGGTCCGGGACAGACTTACCTCACCATCAGTACGTGAG 309
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 61 AspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGln 80

QY 310 CCTGAAGATTTTGACGTGATTACTGTACAGAGTATGTAGGCTCACCTCAGACACTCAG 369
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 81 ProGluAspPheAlaValAlaTyrrTyrcysGlnGlnInTyrglySerSerProArg----- 97

QY 370 ATCACTTTCCGCGAGGAGCAAGGTTGAGATCAACGA 408
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 98 ---ThrPheGlyGlnGlyThrIlyValGluIleLeuArg 109
  
```

## RESULT 9

H44151  
 ig kappa chain V region (UM-15) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 09-Jul-2004  
 C/Accession: H44151  
 R/Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Cauchien, R.H.; Graff, R.; DeGraw, J.; Py  
 Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992  
 A>Title: Human combinatorial antibody libraries to hepatitis B surface antigen.  
 A/Reference number: A44151; PMID:92228746; PMID:1373487



```
QY 130 CTCTCTGAGAGGCCAGTCAAGATTAGAGCTACTTACCTGTGTAACGACGAGAA 189
|||
Db 21 LeuSerCyArGAlaSerGlnSerValSerSerSerTyrLeuAlaTrpTyrGlnGlnAyr 40
|||
QY 190 CCTGGCCAGAGCTCCAGAGCTCCCTCATCTTATGGGATCCACGAGGCGCATGGATGCA 249
|||
Db 41 ProGlyGlnAlaProArgLeuLeuLeuTyrGlyAlaSerSerArgAlaThrGlyLeuPro 60
|||
QY 250 GACAGGTTCAAGTGGAGTGGGTCGCGGACAGACTTCACTTCCATCCATCAGTAGATGGAG 309
|||
Db 61 AspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGln 80
|||
QY 310 CCTGAAGATTTTGCAGTGTATTAATCTGTCAGCAGTATGATAGCTACCTCAGACACTCAG 369
|||
Db 81 ProGluAspPheAlaValTyrTyrCysGlnGlnTyrGlyAlaSerPro----- 96
|||
QY 370 ATCACTTTCGCGGAGGACCAAGGTGAGATCAACGA 408
|||
Db 97 LeuThrPheGlyGlnGlyThrTyrValGlnIleLeuAyr 109
|||
RESULT 12
F30607
Ig kappa chain V-II region (Bor) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C/Accession: F30607
R/Gonm, F.R.; Chen, P.P.; McGinnis, D.; Arjouni, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989
A>Title: Structural and idotypic characterization of the L chains of human Igm autoanti
A:Reference number: A30601, MUID:89215279; PMID:2496160
A:Accession: F30607
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-109 <GON>
A:Cross-references: UNIPROT:Q9UL78
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>
Alignment Scores:
Pred. No.: 8,7e-30 Length: 109
Score: 526.00 Matches: 103
Percent Similarity: 94.69% Conservative: 4
Best Local Similarity: 91.15% Mismatches: 2
Query Match: 30.71% Indels: 1
DB: 2 Gaps: 1
US-09-194-164-13 (1-918) x F30607 (1-109)
QY 70 GATATTGTGTGACGACGCTCCAGGACCCCTGTCTTGTCTTCAGGGGAAAGAGCCACC 129
|||
Db 1 GlnIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGlnArgAlaThr 20
|||
QY 130 CTCTCTGAGAGGCCAGTCAAGATTAGAGCTACTTACCTGTGTAACGACGAGAA 189
|||
Db 21 LeuSerCyArGAlaSerGlnSerValSerSerSerTyrLeuAlaTrpTyrGlnGlnAyr 40
|||
QY 190 CCTGGCCAGAGCTCCAGAGCTCCCTCATCTTATGGGATCCACGAGGCGCATGGATGCA 249
|||
Db 41 ProGlyGlnAlaProArgLeuLeuLeuTyrGlyAlaSerSerArgAlaThrGlyLeuPro 60
|||
QY 250 GACAGGTTCAAGTGGAGTGGGTCGCGGACAGACTTCACTTCCATCCATCAGTAGATGGAG 309
|||
Db 61 AspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGln 80
|||
QY 310 CCTGAAGATTTTGCAGTGTATTAATCTGTCAGCAGTATGATAGCTACCTCAGACACTCAG 369
|||
Db 81 ProGluAspPheAlaValTyrTyrCysGlnGlnTyrGlyAlaSerProGln----- 97
|||
QY 370 ATCACTTTCGCGGAGGACCAAGGTGAGATCAACGA 408
|||
Db 98 ---ThrPheGlyGlnGlyThrTyrValGlnIleLeuAyr 109
|||
```

```
RESULT 13
K3H0HA
Ig kappa chain precursor V-II region (Hah) - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C/Accession: P10022
R/Kips, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A>Title: Autoantibody-associated kappa light chain variable region gene expressed in chr
A:Reference number: P10021; MUID:88171307; PMID:3127527
A:Accession: P10022
A:Molecule type: mRNA
A:Residues: 1-129 <KIP>
A:Cross-references: UNIPROT:P19135
C/Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed i
C/Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kai
hain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 1:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-II region (Hah) #status predicted <MAT>
F:21-117/Region: V segment
F:36-111/Domain: immunoglobulin homology <IMM>
F:44-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-117/Region: complementarity-determining 3
F:118-129/Region: J segment (JK1)
F:43-109/Disulfide bonds: #status predicted
Alignment Scores:
Pred. No.: 8,65e-30 Length: 129
Score: 526.00 Matches: 103
Percent Similarity: 95.58% Conservative: 5
Best Local Similarity: 91.15% Mismatches: 1
Query Match: 30.71% Indels: 4
DB: 1 Gaps: 1
US-09-194-164-13 (1-918) x K3H0HA (1-129)
QY 70 GATATTGTGTGACGACGCTCCAGGACCCCTGTCTTGTCTTCAGGGGAAAGAGCCACC 129
|||
Db 21 GlnIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGlnArgAlaThr 40
|||
QY 130 CTCTCTGAGAGGCCAGTCAAGATTAGAGCTACTTACCTGTGTAACGACGAGAA 189
|||
Db 41 LeuSerCyArGAlaSerGlnSerValSerSerSerTyrLeuAlaTrpTyrGlnGlnAyr 60
|||
QY 190 CCTGGCCAGAGCTCCAGAGCTCCCTCATCTTATGGGATCCACGAGGCGCATGGATGCA 249
|||
Db 61 ProGlyGlnAlaProArgLeuLeuLeuTyrGlyAlaSerSerArgAlaThrGlyLeuPro 80
|||
QY 250 GACAGGTTCAAGTGGAGTGGGTCGCGGACAGACTTCACTTCCATCCATCAGTAGATGGAG 309
|||
Db 81 AspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGln 100
|||
QY 310 CCTGAAGATTTTGCAGTGTATTAATCTGTCAGCAGTATGATAGCTACCTCAGACACTCAG 369
|||
Db 101 ProGluAspPheAlaValTyrTyrCysGlnGlnTyrGlyAlaSerProArg----- 117
|||
QY 370 ATCACTTTCGCGGAGGACCAAGGTGAGATCAACGA 408
|||
Db 118 ---ThrPheGlyGlnGlyThrTyrValGlnIleLeuAyr 129
|||
RESULT 14
S38493
Ig heavy chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
```



C/Accession: S38493  
R.Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Pinnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S  
Submitted to the EMBL Data Library, June 1993  
A/Description: Human antibody fragments specific for human blood group antigens from a B  
A/Reference number: S38493  
A/Accession: S38493  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-123 <MAR>  
A/Cross-References: EMBL:Z23036; NID:g414033; PIDN:CAA80571.1; PID:g414034  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotrimer; Immunoglobulin  
F:15-98/Domain: Immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	1,026-29	Length:	123
Score:	525.00	Matches:	104
Percent Similarity:	87.20%	Conservative:	5
Best Local Similarity:	83.20%	Mismatches:	14
Query Match:	30.65%	Indels:	2
DB:	2	Gaps:	1

US-09-194-164-13 (1-918) x S38493 (1-123)

```
OY 478 CAGGTGACAGCTGTGAGTCTGGGGGAGGCGTGCACGCTGGAGGTCCTGAGACTC 537
DB 1 GlnValGlnLeuGlnGlnSerGlyGlyValValGlnProGlyArgSerLeuSerLeu 20
OY 538 TCCCTGTCAGCCTCTGATTCCTCCCTTCAGAGCTTGTCTATGACATGAGTCCGACGCT 597
DB 21 SerCybAlaIaSerGlyPheSerSerThrAlaMetHisThrValArgGlnAla 40
OY 538 CTAGGCAGAGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGCACTAAATATCATC 657
DB 41 ProGlyLysGlyLeuGlnIleValIleValIleSerTyraPglYSerAsnIleTyThr 60
OY 658 GCAGACTCCGTGAGGGCCGATTCACATCTCCAGAGACACTTCCAGAGACCGGTAT 717
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgPAsnSerIleAsnThrLeuTyR 80
OY 718 CTAAATATGACAGCCTGAGAACTGAGACACGCGCTGTATTAATGTCGAGATCAG 777
DB 81 LeuGlnMetAsnSerLeuArgIaGlnAspThrAlaValIleTyThrCybAlaArgAlaArg 100
OY 778 AGCCTGTTGGTGAATGACCACTACCTACGCTTGGAGCTGGGGCAAGGAGACACG 837
DB 101 SerAsnIlePAsnIleTyR-----TyRThrIleMetAspValIlePglYSerGlyThrThr 118
OY 838 GTACACGCTCTCCTCA 852
DB 119 ValThrValSerSer 123
```

## RESULT 15

S49532  
anti-Sm antibody VL chain (V kappa 3/J kappa 2) - human  
C/Species: Homo sapiens (man)  
C/Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 21-Jan-2000  
C/Accession: S49532  
R/Mamoudi, M.; Edwards, J.; Calins, E.; Bell, D.  
Submitted to the EMBL Data Library, October 1994  
A/Description: Molecular characterization of natural human anti-Sm autoantibodies.  
A/Reference number: S48797  
A/Accession: S49532  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-129 <MAR>  
A/Cross-References: EMBL:Z46345; NID:g560843; PIDN:CAA86464.1; PID:g560844  
F:36-111/Domain: Immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	1,026-29	Length:	129
Score:	525.00	Matches:	103

Percent Similarity:	94.69%	Conservative:	4
Best Local Similarity:	91.15%	Mismatches:	2
Query Match:	30.65%	Indels:	4
DB:	2	Gaps:	1

US-09-194-164-13 (1-918) x S49532 (1-129)

```
OY 70 GATATTGTTTACCGACAGTCTCCAGGACCCCTGTCTTTGTCTCCAGGGAGAGAGCCACC 129
DB 21 GlnIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyIleArgAlaThr 40
OY 130 CTCTCTGAGGGCCAGTCAGAGTGTGTAGCAGCTACTTACCTCGTACAGCAGGAAA 189
DB 41 LeuSerCybArgAlaSerIleSerPheSerSerThrIleValIleValIleValIleVal 60
OY 190 CTGGCCAGGCTCCAGGCTCCTCATCTATGTGTGATCCAGGAGGCGACCTGAGATGCA 249
DB 61 ProGlyGlnAlaProArgLeuLeuIleTyRgIyAlaSerSerArgAlaThrGlyIlePro 80
OY 250 GACAGGTTCAGTGCGAGTGGGTCCGGACAGACTTCACTTCACTCAGATCAGTACTGAG 309
DB 81 AspArgPheSerGlySerGlySerGlyThrAspPheThrIleSerArgLeuGln 100
OY 310 CCTGAAGATTTTGCAGTGTATTACTGTACGACGATATGGAGTCACTCAGACCTCAG 369
DB 101 ProGlnAspPheAlaValIleTyRcybGlnGlnIleTyRgIySerSerProGln----- 117
OY 370 ATCACTTTCGGCGAGGAGCAAGAGGTGAGATCAACGA 408
DB 118 ---ThrPheGlyGlnGlyThrIleLeuGlnIleIleValArg 129
```

Search completed: February 18, 2005, 08:46:50  
Job time : 28 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 18, 2005, 07:22:18 ; Search time 109 Seconds

(without alignments) 8625.481 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 1713  
Sequence: 1 GAATTCATGAAAAAACCGC.....ATCACCATTGTAAGCTT 918

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

MODEL=frame+n2p.model -DEV=xlh  
-O=/cgn2.1/USPTO/spool/US09194164/runat.16022005.122613.6022/app.query.fasta\_1.1095  
-DB=Uniprot\_03 -QFMT=fastaan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human0.cdi -LIST=45  
-DOCCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pct -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09194164@cgn.1.101@runat.16022005.122613.6022 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Uniprot\_03:\*

1: uniprot\_prot:\*\n2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688	40.2	262	2	Q65Z11 mus musculi
2	555	33.4	236	2	Q6P5S8
3	548	33.0	236	2	Q6P1I8
4	547.5	32.0	235	2	Q6GMV9
5	544.5	31.8	235	2	Q6PJP2
6	530	30.9	109	1	Q9UL78
7	526	30.7	129	1	KV3L_HUMAN
8	523	30.5	109	1	KV3B_HUMAN
9	520	30.4	129	1	KV3M_HUMAN
10	515.5	30.1	613	2	Q8WUK1
11	510	29.8	109	1	KV3D_HUMAN
12	506	29.5	109	1	KV3E_HUMAN
13	506	29.5	240	2	Q65ZC9
14	498.5	29.1	122	1	HV3G_HUMAN
15	497	29.0	109	2	Q9UL85
16	493	28.8	116	2	Q9UL93

17	491	28.7	109	1	KV3G_HUMAN	P04206 homo sapien
18	486.5	28.4	147	2	Q9Y5O9	Q9Y5O9 homo sapien
19	484	28.3	108	1	KV3A_HUMAN	P01619 homo sapien
20	480	28.0	113	2	Q9UL90	Q9UL90 homo sapien
21	478	27.9	478	2	Q6P181	Q6P181 homo sapien
22	475	27.7	472	2	Q6N089	Q6N089 homo sapien
23	473.5	27.6	573	2	Q8WU38	Q8WU38 homo sapien
24	470	27.4	100	1	KV3C_HUMAN	P01621 homo sapien
25	468.5	27.3	235	2	Q6GMW0	Q6GMW0 homo sapien
26	467.5	27.3	606	2	Q6GMV2	Q6GMV2 homo sapien
27	466	27.2	236	2	Q6P1H7	Q6P1H7 homo sapien
28	463.5	27.1	122	1	HV3I_HUMAN	P01769 homo sapien
29	463.5	27.1	544	2	Q6P195	Q6P195 homo sapien
30	463	27.0	121	1	HV3J_HUMAN	P01771 homo sapien
31	458.5	26.8	122	2	Q9UL84	Q9UL84 homo sapien
32	457	26.7	597	2	Q96BB9	Q96BB9 homo sapien
33	455	26.6	119	1	HV3I_HUMAN	P01770 homo sapien
34	455	26.6	121	2	Q9UL71	Q9UL71 homo sapien
35	454	26.5	109	2	Q9UL85	Q9UL85 homo sapien
36	451	26.3	493	2	Q8NCL6	Q8NCL6 homo sapien
37	449.5	26.2	128	1	KV3K_HUMAN	P06311 homo sapien
38	449	26.2	109	1	KV3F_HUMAN	P01624 homo sapien
39	449	26.2	493	2	Q68CN4	Q68CN4 homo sapien
40	448.5	26.2	126	1	HV3K_HUMAN	P01772 homo sapien
41	448	26.2	129	1	KV3H_HUMAN	P04207 homo sapien
42	445	26.0	464	2	Q6WZ06	Q6WZ06 homo sapien
43	444	25.9	470	2	Q6PJ44	Q6PJ44 homo sapien
44	443	25.9	519	2	Q6N092	Q6N092 homo sapien
45	442	25.8	482	2	Q7Z351	Q7Z351 homo sapien

## ALIGNMENTS

RESULT 1  
Q65Z11 PRELIMINARY; PRT: 262 AA.  
ID Q65Z11  
AC Q65Z11: 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE Anti-HIV-1 reverse transcriptase single-chain variable.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Hybridoma;  
RX MEDLINE=96211469; PubMed=8648670;  
RA Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;  
RT "Targeting human immunodeficiency virus type 1 reverse transcriptase  
RT by intracellular expression of single-chain variable fragments to  
RT inhibit early stages of the viral life cycle."  
RL J. Virol. 70:3392-3400(1996).  
DR EMBL: U48716; AAB64342.1;  
DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.  
DR InterPro: IPR003599; IG.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003598; IG\_C2.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; IG\_2.  
DR SMART: SM00409; IG\_2.  
DR SMART: SM00408; IG\_C2; 2.  
DR SMART: SM00406; IG\_V; 2.  
DR PROSITE: PS50835; IG\_LIKE; 2.  
KW RNA-directed DNA polymerase.  
SQ SEQUENCE 262 AA; 27842 MW; 7DF20138B53865B4 CRC64;  
Alignment Scores: 4.81e-44 Length: 262  
Pred. No.: 688.00 Matches: 142  
Score: 67.39% Conservative: 44  
Percent Similarity: 51.45% Mismatches: 60  
Best Local Similarity: 51.45%

```

Query Match: 40.16% Indels: 30
DB: 2 Gaps: 6
US-09-194-164-13 (1-918) x Q65ZIL (1-262)

QY 70 GATATTGTTGACGAGCTCTCCAGGACCCCTGTTGTCTCCAGGGGAAGAGCCACC 129
DB 2 APTLLEIEMETHTGINSERPROALATRLIUSERVALTHPRDGLYASPRGVALSER 21
QY 130 CTCTCCGAGGGCCAGTCAAGTGTAGTACAGACTAGTACCTGTAACAGAGAGA 189
DB 22 LEUSERCYARGALASERGINSEITILE---SERASPHELEHISIRPYRGINGINLYS 40
QY 190 CCTGGCCAGGCTCCAGGCTCTCATCTATGCTGATCCACAGGGCCACTGGCATGCA 249
DB 41 SERHLAGLSERPROARGLEULEULELISYTYALASERDINSERLISERGYILEPRO 60
QY 250 GACAGGTTAGTGGGAGTGGTCCGGGAGACAGACTTCACTCCATCCAGTACGAG 309
DB 61 SERARGPHESEIRGLYSERGLYSERGLYSERASPHEHISERLISEASERVALGLN 80
QY 310 CCTGAAGATTTTGCAGTGTATTACTGTCTGACAGATAGTATGATCCACTGACACTCAG 369
DB 81 PROGLIAPRYALGLYVALTYRTYRCYSGINASNGLYHISERPHRO----- 96
QY 370 ATCACTTTGGCGGAGGAGCAAGAGTGAGATCAAGAACTGTGGCTGCACCATCTGTC 429
DB 97 LEUTHRPHAGLYALAGLYTHRILYRGLYGLULYALAGLAAPRALAIPROTHRAL 116
QY 430 TCT-----GGGCGTGGCGGCTCCGGAGGTGGTGGGA 459
DB 117 SERLIEHPHROPROSERSEIRLYSEUGLYPROGLYGLYGLYSEIRGLYGLYGLY 136
QY 460 TCAGGTGAGGTGGC-----TCCAGAGTGCAGGCTGAGTGTGGGGA 504
DB 137 SERGLYGLYGLYSEIRGLYSEUGLYARGSERGLVALGLINLEUNGINSERGLYPRO 156
QY 505 GGGGTGCTCAGCTGGAGGCTCCCTGAGAATCTCTCTGTGACAGCTCTGAGATTCCTTC 564
DB 157 SERLEUVALLYPROSERGINTHIRLEUSERLEUTHRCYSESERVALTHRGLYASPERILE 176
QY 565 AAGAAGTTTGATGATGACGTGGGCGGCGGCTGAGGAGGAGGCTGAGTGGTGGGA 624
DB 177 THIRSEGLYTYRTTRIPASNTIRPLEARGLYSPHEPROGLYASNLYSLEUSPTRYMCGLY 196
QY 625 GTTATATCATATGATGAGAGCACTAAATCTACGACAGACTCCGTGAAGGCGGATTCACC 684
DB 197 TYRILEASNTYRSEIRGLYASPTHIR---TYRTYRASNPROSEIRLEUYSERHAGLIESER 215
QY 685 ATCTCCAGAGACACTTCCAGAGAACAGCGGTGATCTAAATGAACAGCTGAGAACTGAG 744
DB 216 ILETHALASPTHIRSEIRYASNGINTYRTYRLEUGLINLEUSASERVALTHIRTHGLI 235
QY 745 GACAGGCGTGTCTATTACTGTGAGAGATCAGAGGCTGTGGTGATCATATGACACTAC 804
DB 236 ASPALALATHIRTYRYSGLYGLYGLYLEUASPTHIR----- 248
QY 805 TACGTTTGGACGCTCGGGCAAAAGGAGACCGGTCAACGCTCTCTCA 852
DB 249 -----METASPLYRTIRPGLYGLINGLYTHIRSEVALTHIRVALSER 262

RESULT 2
Q6P5S8 PRELIMINARY; PRT; 236 AA.
AC Q6P5S8;
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
OK

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strassberg R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stalcen M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RA Strassberg R.,
RL Submitted (NOV-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC062704; AAH62704.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; Ig_2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ
SEQUENCE 236 AA; 25773 MW; 953B37DEBAF5F27 CRC64;

Alignment Scores:
Pred. No.: 6,66e-34 Length: 236
Score: 555.00 Matches: 126
Percent Similarity: 66.06% Conservative: 18
Best Local Similarity: 57.80% Mismatches: 48
Query Match: 32.40% Indels: 26
DB: 2 Gaps: 6

US-09-194-164-13 (1-918) x Q6P5S8 (1-236)

QY 70 GATATTGTTGACGAGCTCTCCAGGACCCCTGTTGTCTCCAGGGGAAGAGCCACC 129
DB 21 GUILLIVALLERHGLSERPROGLYTHIRLEUSERPHESEPROGLYGLINRGLATNR 40
QY 130 CTCTCCGAGGGCCAGTCAAGTGTAGTACAGACTAGTACCTGTAACAGAGAGA 189
DB 41 LEUSERCYARGALASERGINTHIRVALPHESEIRHISLEUALATIRPYRGINGINAG 60
QY 190 CCTGGCCAGGCTCCAGGCTCTCATCTATGCTGATCCACAGGGCCACTGGCATGCA 249
DB 61 PROGLYGLIAPRALAPROARGLEULEULELISYTYALASERASERARGALATHIRGLYILEPRO 80
QY 250 GACAGGTTAGTGGGAGTGGTCCGGGAGACAGACTTCACTCCATCCAGTACGAG 309
DB 81 ASPARGPHESEIRGLYSERGLYSEIRGLYTHIRAPSPHEHISERLIEHIRTHIRGSEUGLI 100
QY 310 CCTGAAGATTTTGCAGTGTATTACTGTGACAGAGTATGATGATCCACTGACACTCAG 369

```

```

Db      101 ProGluAepPheAlaValTyrPheCysGlnGlnTyrGlyThrSer-----ProSer 117
Qy      370 ATCACTTTCGGCGAGGAGCAAGGTGAATCAACGAACCTGTGCTGCACCATCTGTC 429
      118 LeuThrPheGlyGlyGlyThrArgValGluIleValArgThrValAlaIleProSerVal 137
Qy      430 TCTGGCGGCGGCGGCTCCGAGGTGTGATCAGGTGAGAGTGCTCCAGGTCAGCTG 489
      138 -----PheIlePheProProSerAspGlnGlnLeu 147
Qy      490 GTGAGTCTGGGAGGCGGTGTCAGCTGGAGAGTCCCTGAGACTCTCTGTGACGCC 549
      148 IysSerGlyThrAlaSerValVal-----CysLeuLeu 158
Qy      550 TCTGATTCCTCCCTTCAGAGCTTTGCTATGACCTGG---GTCCGCGAGGCTCTAGGCAAG 606
      159 AenAenPheTyrProArgGlnAlaValGlnTyrValAlaPheAenAlaLeuGlnSer 178
Qy      607 GGGCTGAGTGGGTGCACTTATATCATATGATGAGACACTTAATCAACGACACTCC 666
      179 GlyAenSerGlnGlnSerValThrGlnAenSerLysAspSerThrTyr-----Ser 196
Qy      667 GTGAAGGCGCGATTCACATCTCCAGA---GACACTTCAGAGAACAGCGGTAT 717
      197 LeuSerSerThrLeuThrLeuSerLysAlaAepTyrGlnLysHisLysValTyr 214

RESULT 3
Q6PIL8 PRELIMINARY; PRT; 236 AA.
ID      06PIL8
AC      05-JUL-2004 (TREMBLrel. 27, Created)
DT      05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
      Altschul S.F., Collins F.S., Wagner L., Shemmen C.M., Schaller G.D.,
      Hopkin R.F., Jordan K.H., Moore T., Max S.I., Wang J., Hsieh F.,
      Diczchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
      Brownstein M.T., Ustin T.B., Toshlyuk S., Carninci P., Frange C.,
      Raha S.S., Loguillano N.A., Peters G.J., Abramson R.D., Miallhy S.J.,
      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
      Villalón D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
      Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
      Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
      Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
      Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
      Jones S.J., Marra M.A.;
      "Generation and initial analysis of more than 15,000 full-length human
      and mouse cDNA sequences,"
      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      Strauberg R.;
      Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC032451; AAH32451.1; -.
DR      HSSP; P01837; IKCU.
DR      InterPro; IPR003599; IG.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003597; IG cl.
DR      InterPro; IPR003006; IG_MHC.

```

```

DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF07654; CI-secl; I.
DR      SMART; SM00409; IG; 2.
DR      SMART; SM00407; IGcl; 1.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PSS0835; IG_LIKE; 2.
DR      PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
DR      Hypothetical protein.
SQ      SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Alignment Scores:
Pred. No.:      2,28e-33      Length:      236
Score:          548.00      Matches:      127
Percent Similarity: 65.28%      Conservative: 14
Best Local Similarity: 58.80%      Mismatches: 49
Query Match:    31.99%      Indels:      26
DB:              2      Gaps:      6

US-09-194-164-13 (1-918) x Q6PIL8 (1-236)
Qy      76 GTGTTGACGCACTCTCCAGCACCTGTCTTGTCTCCAGGGAGAAAGACCCCTCTCC 135
      23 ValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGlnArgAlaThrLeuSer 42
Qy      136 TCGAGGCGCCAGTCAAGAGTTGTAGACACTTACCTTACCTGGTACCAAGAAACCTGGC 195
      43 CysArgAlaSerGlnSerLeuSerSerSerTyrLeuAlaTyrGlnGlnLysProGly 62
Qy      196 GAGGCTCCCGAGGCTCTCTCATATGATGATCACACGAGGCGCACTGGAGTGCAGACAG 255
      63 GlnAlaProArgLeuLeuLeuTyrGlyValSerSerArgAlaThrGlyLeuProAspArg 82
Qy      256 TTCAGTGGCAGTGGGTCCGCGAGCAAGACTTCACTTCACCATGAGTACAGTGCAGTGA 315
      83 PheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGlnProGlu 102
Qy      316 GATTTTGCAGTGTATTATCTGTACAGAGTATGTGTAGTCACTCAACAGACTCAAGATCACT 375
      103 AepPheAlaValTyrTyrCysGlnGlnTyrGlyThrSer-----ArgProIleThr 119
Qy      376 TTGGCGGAGGAGGAGCAAGCATGAGATCAACAGCACTGGTGCACCATCTGCTGTGCG 435
      120 PheGlyGlnGlyThrArgLeuAspIleLysArgThrValAlaIleProSerVal----- 137
Qy      436 GGTGGCGGTTCCGAGAGTGTGATCAGGTGAGGTGCTCCAGGTGCAAGCTGTGTGAG 495
      138 -----PheIlePheProProSerAspGlnGlnLysSer 149
Qy      496 TTTGGGAGGAGGCGGTGCTCCAGCTGGAGAGTCCCTGAGACTCTCTGTGACGCTTGA 555
      150 GlyThrAlaSerValVal-----CysLeuLeuAenAen 160
Qy      556 TTCCCTCCAGAGAGCTTGTCTATGACCTGG---GTCCGCGAGGCTCTAGCAAGGCGTGC 612
      161 PheTyrProArgGlnAlaLysValGlnTyrValAlaPheAenAlaLeuSerGlyAen 180
Qy      613 GAGTGGTGGCGATTATATCATATGATGAGACACTTAATACATGACAGCTCCGTAAG 672
      181 SerGlnGlnSerValThrGlnGlnAenSerLysAspSerThrTyr-----SerLeuSer 198
Qy      673 GGGCAATTCACCATCTCCAGA---GACACTTCAGAGAACAGCGGTAT 717
      199 SerThrLeuThrLeuSerLysAlaAepTyrGlnLysHisLysValTyr 214

RESULT 4
Q6GMV9 PRELIMINARY; PRT; 235 AA.
ID      06GMV9
AC      05-JUL-2004 (TREMBLrel. 27, Created)
DT      05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).

```

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Primates; Catarrhini; Hominiidae; Homo.  
XX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,  
RA Datchenko L., Marsina K., Farmer A.A., Rubin G.W., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein W.J., Udell T.B., Toshlyuki S., Carninci P., Frange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallatou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard J.,  
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalka U., Smallos D.E., Schmerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences." ;  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) .  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Straubeberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.  
RL EMBL; BC073793; AAH73793.1; -.  
DR InterPro: IPR003599; IG\_  
DR InterPro: IPR007110; IG\_Like.  
DR InterPro: IPR003597; IG\_C1.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam; PF07654; Cl-set; 1.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; Ig; 2.  
DR SMART; SM00407; IGCL; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 235 AA; 25646 MW; DF3B56BAD19E4B CRC64;

QY	310	CCCTGAAGATTTTTCAGCTGATATTAATCTGACGAGTATGGTATGACACTGACACCTCAG	369
QY	310	CCCTGAAGATTTTTCAGCTGATATTAATCTGACGAGTATGGTATGACACTGACACCTCAG	369
Db	101	SergIuaSepheAlaLeuIyrTheCySgInGInIYrGlyThnSerPro	116
QY	370	ATCATCTTCGCGGAGGAGACCAAGGTGAGATCAACAGACTGTGCTGCACCATCTGTC	429
Db	117	LeuthrPheGlyGlyGlyThrIySValGluIeIyBaSgThnValAlaIaIaProSerVal	136
QY	430	TCTGGCGGCTGGCGGTTCCGAGAGGTGTGATGAGTGCAGGTGGCTCCAGGTGCAGCTG	489
Db	137	-----PheIlePheProProSerAspIugInIleu	146
QY	490	GTGAGCTCTGGGGGAGGCGGTGGCTCCAGCCTGGAGAGTCCCTGAGACTCTCGTGCAGCC	549
Db	147	LySserGlyThnAlaIaSerValVal	157
QY	550	TCTGGAATTCCTCCCTCAGAAAGCTTTGTCTATGCACTGG--GTCCGCGAGCGCTTGAAGCAAG	606
Db	158	AsnAenPheIyYrProAygGluIaIaIySValGInItrIplySValAspAenAlaIeuGInSer	177
QY	607	GGCGTGGAGTGGGTGCGAGCTTATATCATATATGATGAGAAGACTTAATATCAAGCAAGCTCC	666
Db	178	GlyAenSerGInIugIuSerValThrGInIuAenSerIySAspSerThrIyYr	195
QY	667	GTGAAGGGCGCGCATTCACCATCTCCAGA---GACACTTCCAAAGACACGGTGTAT	717
Db	196	LeuSerSerThnLeuthrIleuSerIySAlaAspIyRGIuIySAlaIySValIyR	213
RESULT 5			
Q6PUF2			
AC	Q6PUF2	PRELIMINARY;	PRT; 235 AA.
DT	05-JUL-2004 (TREMBlrel. 27, Created)		
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)		
DE	Hypothetical protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,		
RA	Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.J., Ruben G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carlinici P., Prance C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abraham R.D., Mullany S.J.,		
RA	Bozak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Kirylushina M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Maris M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung;		
RL	Straubeberg R.;		
DR	EMBL; BC016380; AAH16380.1; --		
DR	HSSP; P01837; IKCU.		
DR	InterPro; IPR003599; IG.		

RESULT 5	06RUF2	PRELIMINARY:	PRT:	235 AA.
ID	06RUF2			
AC	06RUF2			
DT	05-JUL-2004	(TREMBLrel. 27, Created)		
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)		
DE		Hypothetical protein.		
OS		Homo sapiens (Human).		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX		NCBI_TaxID=9606;		
RN		[1]		
RP		SEQUENCE FROM N.A.		
RC		TISSUE=Lung;		
RC		MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA		Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA		Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,		
RA		Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,		
RA		Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA		Datchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,		
RA		Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA		Brownstein M.J., Usdin T.B., Toshiyuki S., Carncini P., Prange C.,		
RA		Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollaby S.J.,		
RA		Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA		Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA		Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA		Fahney U., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA		Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA		Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA		Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA		Kryzhanik M.I., Skalske U., Smatius D.E., Scherch A., Schein J.E.,		
RA		Jones S.J., Marra M.A.;		
RT		"Generation and initial analysis of more than 15,000 full-length human		
RT		and mouse cDNA sequences."		
RL		Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN		[2]		
RP		SEQUENCE FROM N.A.		
RC		TISSUE=Lung;		
RA		Straubeberg R.,		
RA		Submitted (Oct-2001) to the EMBL/Genbank/DBJ databases.		
DR		EMBL; BC016380; AAHL6380.1; -.		
DR		HSSP; P01837; IKCU.		
DR		InterPro; IPR003599; IG.		

DR InterPro: IPR007110; Ig-1like.  
 DR InterPro: IPR003587; Ig\_C1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF07654; C1-set; 1.  
 DR SMART: SM00409; Ig; 2.  
 DR SMART: SM00407; IgC1; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00835; IG\_LIKE; 2.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
 DR Hypothetical protein.  
 SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

## Alignment Scores:

Pred. No.:	4,21e-33	Length:	235
Score:	544.50	Matches:	127
Percent Similarity:	65.14%	Conservative:	15
Best Local Similarity:	58.26%	Mismatches:	49
Query Match:	31.79%	Indels:	27
DB:	2	Gaps:	6

US-09-194-164-13 (1-918) x Q6PUF2 (1-235)

```

QY 70 GATATTGTTGAGCCAGCTCCAGGACCCGTGTTGTCTCCAGGGGAAAGGCCACC 129
DB 21 GIUIEVALLeuThnGlnSerProAlaThrLeuSerLeuSerProGlyGlnArgAlaThr 40
QY 130 CTCTCTCCAGGGCCAGCTCAGAGTGTAGTACAGCTACTGACCTGAGCAGAGAA 189
DB 41 LeuSerCybArgAlaSerGlnLeuAlaSerSerAlaTyLeuAlaThrTyArgGlnGln 60
QY 130 CTTGGCCAGGCTCCAGGCTCTCATCTATGGTGCATTCACAGGCGCCACTGGCATGCCA 249
DB 61 ProGlyGlnAlaProArgLeuLeuMetPheGlySerSerArgAlaThrGlyLeuPro 80
QY 250 GACAGGTCAGTGGAGGAGTGGTCCGGGAGACACTTCACCTCAGACATGATGATGAG 309
DB 81 AsparGpneSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGln 100
QY 310 CCTGAAGATTGTGACGTATTACTGTGCAGCAGTATGATGAGTCACTCCAGACCTCAG 369
DB 101 ProGlnAspPheAlaValTyThrCysGlnGlnTyArgIleSerSer-----Gln 116
QY 370 ATCATCTTTCGGCGGAGGAGCCAGGTGAGATCAACAGAACTGTGGCTGCACCATCTGTC 429
DB 117 GlyThrPheGlyProGlyThrIleValAspIleLeuValArgThrValAlaAlaProSerVal 136
QY 430 TCTGCGGAGTGGCGGCTTCCGGAGGTGTGATCAGGTGAGAGTGGCTCCAGGTGAGCTG 489
DB 137 -----PheIlePheProProSerAspGlnGlnLeu 146
QY 490 GTGAGTCTGGGGGAGGCGGTGCTCCAGCTCGGAGAGTCCCTGAGACTCTCTGTGCAGCC 549
DB 147 LysSerGlyThrAlaSerValVal-----CysLeuLeu 157
QY 550 TCTGATTCCTCTTCAAGAGCTTTGCTATGACTGG--GTCCGCGAGGCTCTTAAGCGAAG 606
DB 158 AsnAspPheTyProArgGlnAlaValAlaValGlnTrpValAlaAspAsnAlaLeuGlnSer 177
QY 607 GGGCTGAGTGGGAGGAGTATATCATATGATGAGAGACTAAATATACAGCAGACTCC 666
DB 178 GlnAsnSerGlnGlnSerValThrGlnAspSerLysAspSerThrTy-----Ser 195
QY 667 GTGAAGGCGCAGTTCACATCTCCAGA--GACACTTCCAGAGACAGGTGTAT 717
DB 196 LeuSerSerThrLeuThrLeuSerLysAlaAspTyArgIleValIleValTy 213

```

## RESULT 6

Q9UL78 PRELIMINARY; PRT; 109 AA.

AC Q9UL78; ID Q9UL78; DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

```

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Myosin-reactive Immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL, AF035036; AAD56272.1; -.
DR PIR: A30601; A30601.
DR PIR: A30608; A30608.
DR PIR: B30601; B30601.
DR PIR: B30607; B30607.
DR PIR: C30601; C30601.
DR PIR: C30607; C30607.
DR PIR: C30608; C30608.
DR PIR: D30601; D30601.
DR PIR: D30607; D30607.
DR PIR: D30608; D30608.
DR PIR: F30607; F30607.
DR PIR: F30608; F30608.
DR PIR: G30601; G30601.
DR PIR: G30608; G30608.
DR PIR: H30607; H30607.
DR PIR: H30608; H30608.
DR PIR: H4151; H4151.
DR PIR: I30601; I30601.
DR PIR: PH0963; PH0963.
DR PIR: PH0964; PH0964.
DR PIR: PH0965; PH0965.
DR PIR: S33988; S33988.
DR PIR: S34096; S34096.
DR HSP; P01625; IER3.
DR InterPro: IPR007110; Ig-1like.
DR InterPro: IPR003596; Ig_v.
DR PROSITE: PS00835; IG_LIKE; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EB197 CRC64;

```

## Alignment Scores:

Pred. No.:	4,82e-32	Length:	109
Score:	530.00 <td>Matches: <td>104</td> </td>	Matches: <td>104</td>	104
Percent Similarity:	95.58% <td>Conservative: <td>4</td> </td>	Conservative: <td>4</td>	4
Best Local Similarity:	92.04% <td>Mismatches: <td>1</td> </td>	Mismatches: <td>1</td>	1
Query Match:	30.94% <td>Indels: <td>4</td> </td>	Indels: <td>4</td>	4
DB:	2	Gaps: <td>1</td>	1

US-09-194-164-13 (1-918) x Q9UL78 (1-109)

```

QY 70 GATATTGTTGAGCCAGCTCCAGGACCCGTGTTGTCTCCAGGGGAAAGGCCACC 129
DB 1 GIUIEVALLeuThnGlnSerProGlyThrLeuSerLeuSerProGlyGlnArgAlaThr 20
QY 130 CTCTCTCCAGGGCCAGCTCAGAGTGTAGTACAGCTACTGACCTGAGCAGAGAA 189
DB 21 LeuSerCybArgAlaSerGlnSerValSerSerTyLeuAlaThrTyArgGlnGln 40
QY 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGGTGCATTCACAGGCGCCACTGGCATGCCA 249
DB 41 ProGlyGlnAlaProArgLeuLeuMetPheGlySerSerArgAlaThrGlyLeuPro 60
QY 250 GACAGGTCAGTGGAGGAGTGGTCCGGGAGACACTTCACCTCAGACATGATGAG 309
DB 61 AsparGpneSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGln 80

```

```

QY 310 CCTGAAGATTTCAGGTGATTACTGTGCAGAGTATGTAGTCACTCAGACACCTCAG 369
DB 81 ProgiuaapCyalaValTyrTyrCysgingIntYrGlySerSerPro----- 96
QY 370 ATCAGCTTTGGGGGAGGAGCCAGAGTGGAGATCAACGA 408
DB 97 LeuthrPhegIyGlyGlyThryrValGluIleLysArg 109

RESULT 7
KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region HAH precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=68171307; PubMed=3127527;
RA Kippes T.J., Tomhave R., Chen P.P., Carson D.A.;
RT "Anticombodly-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: The protein is one of the surface immunoglobulin M
CC autointibodies expressed in patients with chronic lymphocytic
CC leukemia.
DR PIR; P10022; K3H0HA.
DR HSSP; P01625; 1EQ.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 129 Ig kappa chain V-III region HAH.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 55 Complementarity-determining-1.
FT DOMAIN 56 70 Framework-2.
FT DOMAIN 71 77 Complementarity-determining-2.
FT DOMAIN 78 109 Framework-3.
FT DOMAIN 110 118 Complementarity-determining-3.
FT DISULFID 43 109 Cys segment.
FT NON_TER 129 129 By similarity.
SQ SEQUENCE 129 AA; 14073 MW; D3CS529277274D0 CRC64;

Alignment Scores:
Pred. No.: 9.97e-32 Length: 129
Score: 526.00 Matches: 103
Percent Similarity: 95.58% Conservative: 5
Best Local Similarity: 91.15% Mismatches: 1
Query Match: 30.71% Indels: 4
DB: 1 Gaps: 1

US-09-194-164-13 (1-918) x KV3L_HUMAN (1-129)
QY 70 GATATTGTTGACGAGCTCCAGGACCCCTGCTTGTCTCCAGGGGAAAGACGACC 129
DB 21 GuileValIeuthrGlnSerProGlyThrLeuSerLeuSerProGlyIuValGalaThr 40
QY 130 CTCTCTGAGGGCCAGTGCAGAGTGTAGTAGAGCTACTAGCTTGATGATCCAGCAGAAA 189
DB 41 LeuSerCyArGAlaSerGlnSerValSerSerSerTyrLeuAlaTrpTyrGlnGlnLys 60

```

```

QY 190 CTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGGCCAGTGGATGCCA 249
DB 61 ProgiyGlnAlaProArGLeuLeuIleTyrGlyAlaSerSerArGAlaThrGlyIlePro 80
QY 250 GACAGGTTCAAGTGGAGGAGGCGGAGCAGACTCAGCTTCACATCAGTAGTAGTGAG 309
DB 81 AsparGlnSerGlySerGlySerGlyThrAspPheThrIleSerArgLeuGln 100
QY 310 CCTGAAGATTTCAGGTGATTACTGTGCAGAGTATGTAGTCACTCAGACACCTCAG 369
DB 101 ProgiuaapPheAlaValTyrTyrCysgingIntYrGlyThrSerProArg----- 117
QY 370 ATCAGCTTTGGGGGAGGAGCCAGAGTGGAGATCAACGA 408
DB 118 ---ThrPheGlyGlnGlyThryrValGluIleLysArg 129

RESULT 8
KV3B_HUMAN
ID KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-III region SIE.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human Igm anti-gamma-globulins of the wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: This chain was isolated from an Igm with anti-gamma
CC globulin activity.
DR PIR; A01892; K3H0SI.
DR HSSP; P01625; 1LVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109 109 By similarity.
SQ SEQUENCE 109 AA; 11775 MW; 7689C3BCD646FFB4 CRC64;

Alignment Scores:
Pred. No.: 1.65e-31 Length: 109
Score: 523.00 Matches: 102
Percent Similarity: 95.58% Conservative: 6
Best Local Similarity: 90.27% Mismatches: 1
Query Match: 30.53% Indels: 4
DB: 1 Gaps: 1

US-09-194-164-13 (1-918) x KV3B_HUMAN (1-109)
QY 70 GATATTGTTGACGAGCTCCAGGACCCCTGCTTGTCTCCAGGGGAAAGACGACC 129
DB 1 GuileValIeuthrGlnSerProGlyThrLeuSerLeuSerProGlyIuValGalaThr 20
QY 130 CTCTCTGAGGGCCAGTGCAGAGTGTAGTAGAGCTACTAGCTTGATGATCCAGCAGAAA 189
DB 21 LeuSerCyArGAlaSerGlnSerValSerArSerTyrLeuAlaTrpTyrGlnGlnLys 40
QY 190 CTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGGCCAGTGGATGCCA 249

```



```
Db 41 ProGlyGlnAlaProArgLeuLeuIleTyrGlyAlaSerSerArgAlaThrGlyIlePro 60
QY 250 GACAGCTTCAGTGGAGAGTGGTCCGGGACAGACTTCACCTCAGATCAGTGGAG 309
Db 61 AsparGpneSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerTrgLeuGln 80
QY 310 CCTGAAGATTTCAGTGTATTACTGTGCAGAGTATGTAGTCACTCAGACCTCAG 369
Db 81 ProAspAspPheAlaValTyrTyrCysGlnGlnTyrGlySerSerProGln----- 97
QY 370 ATCACTTTCCGGCGAGGAGCAAGGTGAGATCAACCA 408
Db 98 ---ThrPheGlyGlnGlySerIleValGlnIleLysArg 109

RESULT 9
KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISBASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
CC PIR; P10021; K3H0H1.
DR HSP; P01625; 1E80.
DR GO; GO:0005576; Cxcracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL.
FT CHAIN 1 20 Ig kappa chain V-II region HIC.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 55 Complementarity-determining-1.
FT DOMAIN 56 70 Framework-2.
FT DOMAIN 71 77 Complementarity-determining-2.
FT DOMAIN 78 109 Framework-3.
FT DOMAIN 110 118 Complementarity-determining-3.
FT DOMAIN 119 129 Jkl segment.
FT DISULFID 43 109 By similarity.
FT NON_TER 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2B74D6 CRC64;
```

## Alignment Scores:

```
Pred. No.: 2,86e-31 Length: 129
Score: 520.00 Matches: 103
Best Local Similarity: 93.81% Conservative: 3
Best Local Similarity: 91.15% Mismatches: 3
Query Match: 30.36% Indels: 4
Gaps: 1
```

US-09-194-164-13 (1-918) x KV3M\_HUMAN (1-129)

QY 70 GATATTGTTGACGACGAGTCTCCAGGACCCCTGTTCTTCTTCACGGGAAAGACCCACC 129

```
Db 21 GlnIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGlnArgAlaThr 40
QY 130 CTTCTCTCAGAGGCGAGTCCAGAGTGTAGTACACTTACCTTACCTGATCAGAGAA 189
Db 41 LeuSerCyArGAlaIleSerGlnSerValSerSerTrgLeuAlaTrpTrgIleGlnLys 60
QY 190 CTTGAGCAGGCTCCAGGCTCCTCATCTATGTGATCACCAGGAGCCATGGCATGCCA 249
Db 61 ProGlyGlnAlaProArgLeuLeuIleTyrGlyAlaSerSerArgAlaThrGlyIlePro 80
QY 250 GACAGCTTCAGTGGAGAGTGGTCCGGGACAGACTTCACCTCAGATCAGTGGAG 309
Db 81 AsparGpneSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerTrgLeuGln 100
QY 310 CCTGAAGATTTCAGTGTATTACTGTGCAGAGTATGTAGTCACTCAGACCTCAG 369
Db 101 Pro***AspPheAlaValTyrTyrCysGlnGlnTyrGlySerSerProTrp----- 117
QY 370 ATCACTTTCCGGCGAGGAGCAAGGTGAGATCAACCA 408
Db 118 ---ThrPheGlyGlnGlySerIleValGlnIleLysArg 129

RESULT 10
Q8WUK1 PRELIMINARY; PRT; 613 AA.
ID Q8WUK1;
AC Q8WUK1;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen G.M., Schler G.D.,
RA Altchul S.F., Zeeberg B., Burow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stalcenon M., Soares M.B., Bonaldo M.F., Cavaant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz U., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR PIR; P36005; P36005.
DR PIR; G36005; G36005.
DR PIR; PH1642; PH1642.
DR PIR; PH1643; PH1643.
DR PIR; PH1645; PH1645.
DR PIR; PH1646; PH1646.
DR PIR; P10098; P10098.
DR PIR; P10120; P10120.
```

DR PIR; S15590; S15590.  
 DR PIR; S31116; S31116.  
 DR PIR; S31119; S31119.  
 DR PIR; S70442; S70442.  
 DR HSSP; P01861; IADQ.  
 DR Pfam; PF07654; Cl-set; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; P500835; IG\_LIKE; 5.  
 DR PROSITE; P500290; IG\_MHC; UNKNOWN 3.  
 DR SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;

## Alignment Scores:

Pred. No.:	7,9e-31	Length:	613
Score:	515.50	Matches:	101
Percent Similarity:	85.04%	Conservative:	7
Best Local Similarity:	79.53%	Mismatches:	14
Query Match:	30.09%	Indels:	5
DB:	2	Gaps:	1

US-09-194-164-13 (1-918) x Q8WUK1 (1-613)

QY 478 CAGGTGACGCTGTGAGTCTGTGGGAGGCGTGTCCAGCTGGAGGTCCTGAGACTC 537  
 DB 20 GlnValGlnLeuValGlnSerGlyGlyValGlnProGlyArgSerLeuArgLeu 39  
 QY 538 TCCTGTGACGCTGTGAGTCTGTGGGAGGCGTGTCCAGCTGGAGGTCCTGAGACTC 597  
 DB 40 SerCybAlaAlaSerGlyPheThrPheSerSerTyGlyMetHisTrpValArgGlnAla 59  
 QY 538 CTAGGCAAGGGGCTGAGTGTGGGAGGCGTGTATATATATATATATATATATATAT 657  
 DB 60 ProGlyGlyGlyLeuGlnLutryPalaAlaValIleSerTyAspGlySerAsnIleTyTr 79  
 QY 658 GCAGACTCCGTGAAGGCGGATTCACCATCTCCAGAGACCTTCCAGAACCGGTGAT 717  
 DB 80 AlaAspSerValIleGlyArgPheThrIleSerArgAspAsnSerIleAsnThrLeuTy 99  
 QY 718 CTTAAATATGAAGCGCTGAGTGTGGGAGGCGTGTATATATATATATATATATAT 777  
 DB 100 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValIleTyTrGlyAlaIleAspTrp 119  
 QY 778 AGCTGTGTGGTGAAGTATGACCACTACGCTGTGGGAGGCGTGTATATATATAT 837  
 DB 120 Ser-----GlnGlyValGlnLutryPheAspIleTrpGlyGlnGlyThrMet 134  
 QY 838 GTACCCGTCTCTCAGGATCC 858  
 DB 135 ValThrValSerSerGlySer 141

## RESULT 11

KV3D\_HUMAN STANDARD; PRT; 109 AA.  
 AC P01622;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig kappa chain V-II region Ti.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=7218439; PubMed=5027703;  
 RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein  
 RT Ti). IV. The complete amino acid sequence and its significance for the  
 RT mechanism of antibody production.";  
 RL Hope-Seyler Z. Physiol. Chem. 353:189-208(1972).  
 CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
 DR PIR; A01895; K3HUTI.

DR HSSP; P01625; 1LVE.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; P500835; IG\_LIKE; 1.  
 DR Bence-Jones protein; Direct protein sequencing;  
 KW Immunoglobulin V region.  
 FT DISULFID 23 89  
 FT NON TER 109 109  
 SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDD7749BC CRC64;

## Alignment Scores:

Pred. No.:	1,62e-30	Length:	109
Score:	510.00	Matches:	100
Percent Similarity:	93.81%	Conservative:	6
Best Local Similarity:	88.50%	Mismatches:	3
Query Match:	29.77%	Indels:	4
DB:	1	Gaps:	1

US-09-194-164-13 (1-918) x KV3D\_HUMAN (1-109)

QY 70 GATATTGTGAGCAGGAGTCTCCAGGACCCGTCCTTGTCTCCAGGGGAAAGGCCACC 129  
 DB 1 GlnIleValIleThrGlnSerProGlyThrLeuSerLeuSerProGlyGlnArgAlaThr 20  
 QY 130 CTCTCTCAGAGGCGCAGTCAAGTGTGTAGCAGCTACTTATAGCTGTATCCAGAGAAA 189  
 DB 21 LeuSerCybArgAlaSerGlnSerValSerAsnSerPheLeuAlaIleTrpGlnGln 40  
 QY 190 CTTGCGCAGGCTCCAGGCTCTCATCTATGTGTGATCACCAGGGCCACTGGCATGCCA 249  
 DB 41 ProGlyGlnAlaProArgLeuLeuIleTyValAlaSerSerArgAlaThrGlyIlePro 60  
 QY 250 GACAGGTTCAAGTGTGGGAGGCGTGTGGGAGGCGTGTATATATATATATATATAT 309  
 DB 61 AsparGlnSerSerGlySerGlySerGlyThrAspPheThrIleSerArgLeuGln 80  
 QY 310 CTTGAAGATTTTGGAGTGTATATATATATATATATATATATATATATATATAT 369  
 DB 81 ProGlnAspPheAlaValIleTyTrCysGlnGlnIleTySerSerProSer----- 97  
 QY 370 ATCACTTTGCGGCGGAGGAGCAAGGTGAGATCAACGA 408  
 DB 98 ---ThrPheGlyGlnGlyThrIleValGlnLeuLysArg 109

## RESULT 12

KV3E\_HUMAN STANDARD; PRT; 109 AA.  
 AC P01623;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig kappa chain V-II region WOL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=82046598; PubMed=6794615;  
 RA Andrews D.W., Capra J.D.;  
 RT "Amino acid sequence of the variable regions of light chains from two  
 RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa  
 RT group.";  
 RL Biochemistry 20:5816-5822(1981).  
 CC -I- MISCELLANEOUS: This chain was isolated from an Igm with anti-gamma  
 DR PIR; A01896; K3HUTL.  
 DR HSSP; P01625; 1LVE.

```

DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; P:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region.
FT DISULFID 23
FT NON TER 89
FT TER 109
SQ SEQUENCE 109 AA; 11746 MW; 566C15B6B9CBEE CRC64;

Alignment Scores:
Pred. No.: 3.27e-30 Length: 109
Score: 506.00 Matches: 100
Percent Similarity: 92.04% Conservative: 4
Best Local Similarity: 88.50% Mismatches: 5
Query Match: 29.54% Indels: 4
DB: 1 Gaps: 1

US-09-194-164-13 (1-918) x KV3E_HUMAN (1-109)
QY 70 GATATTGTTGACGAGCTCCAGGACCCCTGTTGTCCTCAGGGGAAAGCCACC 129
DB 1 GlnIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyValArgAlaThr 20
QY 130 CTCTCTCGAGGCGCAGTCAGAGTGTAGTACAGCTACTTACCTGTGATCCAGAGAA 189
DB 21 LeuSerCybArgAlaSerGlnSerValSerSerGlyTyrLeuGlyTyrPyrGlnGln 40
QY 190 CTGGCCAGGCTCCAGGCTCTCTCATCTATGGTGATCCACAGGCGCCATGGCATGCCA 249
DB 41 ProGlyGlnAlaProArgLeuLeuLeuTyrGlyAlaSerSerArgAlaThrGlyLeuPro 60
QY 250 GACGATTCAGTGGAGAGTGGTCCGGGACAGACTTCACCTCAGCATGAGTGGAG 309
DB 61 AsparGlnSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeuGln 80
QY 310 CCTGAAGATTTCAGTGTATTACTGTGACAGATAGTGTAGTCACTCAGACCTCAG 369
DB 81 ProGlnAspPheAlaValTyrTyrCysGlnGlnTyrGlySerLeuGlyArg----- 97
QY 370 ATCACTTTCCGGCGGAGGACCAAGGTGGAGATCAAAACA 408
DB 98 ---ThrPheGlyGlnGlyThrIleValGlnIleLeuValArg 109

RESULT 13
Q65ZC9 PRELIMINARY; PRT; 240 AA.
AC Q65ZC9;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=bcFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RU Nat. Biotechnol. 15:629-631(1997).
DR EMBL: Y13056; CAA73499.1; -.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig 2.
DR SMART: SM00409; IG; 2.

```

```

DR SMART: SM00406; IGV; 2.
DR PROSITE: PS50835; IG_LIKE; 2.
FT NON TER 1
FT NON TER 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F6AB373 CRC64;

Alignment Scores:
Pred. No.: 3.66e-30 Length: 240
Score: 506.00 Matches: 101
Percent Similarity: 84.13% Conservative: 5
Best Local Similarity: 80.16% Mismatches: 12
Query Match: 29.54% Indels: 8
DB: 2 Gaps: 2

US-09-194-164-13 (1-918) x Q65ZC9 (1-240)
QY 478 CAGGTGACGCTGTGATGCTGGGAGAGCGCTGACGCTGGAGGTCCTGAGATC 537
DB 1 GlnValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20
QY 538 TCTGTGACGCTGTGATTCCTTCAGAACCTTGTCTATGCACTGGTCCGACGCT 597
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrGlyMetIleTyrValArgGlnAla 40
QY 598 CTAGGCAAGGCGCTGAGTGGGTGACATTATATCATATGATGAGACACTAAATATAC 657
DB 41 ProGlyValGlyLeuGlnTyrValAlaValIleSerTyrAspGlySerAsnIleTyr 60
QY 658 GCAGACTCCGAGAGGCGCGATTCACATCTCCAGAGACACTCCAGAACAGGCTGTAT 717
DB 61 AlaAspSerValValGlyAlaArgPheThrIleSerArgAspAsnSerLeuThrLeuTyr 80
QY 718 CTAAATAATGAACGCTGAGAACTGAGAGACAGCGCTGTCTATTACTGTGCGAGATCAG 777
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspPheThrAlaValTyrTyrCysAlaIleArgAsp 99
QY 778 AGCTGTGGTGATATAGACACACTAGCGTTTGACAGCTGTGGGCGAAAGGACCAAG 837
DB 100 -----TyrGlyAsp-----SerLeuAspProTyrGlyValGlyThrLeu 112
QY 838 GTACCGTCTCCTCAGGA 855
DB 113 ValThrValSerSerGly 118

RESULT 14
HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain: location of a possible CH segment.";
RU Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MISCELLANEOUS: This mu chain was isolated from the plasma of a patient with macroglobulinemia.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02051; M3HRAM.
DR HSSP: P01772; 2FB4.
DR GO:0005576; C:extracellular; NAS.
DR GO:0003823; P:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.

```

DR Pfam: PF00047; Ig: 1.  
 DR SMART: SM00406; IGV: 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 DR Direct protein sequencing; Immunoglobulin V region;  
 KW Pyrolydione carboxylic acid.  
 FT MOD RES 1 112 Ig-like.  
 FT NON\_TER 1 122 Pyrolydione carboxylic acid.  
 SQ SEQUENCE 122 AA; 13666 MW; A42D0F17D352F1C2 CRC64;

Alignment Scores:  
 Pred. No.: 1,24e-29 Length: 122  
 Score: 498.50 Matches: 93  
 Percent Similarity: 86.40% Conservative: 15  
 Best Local Similarity: 74.40% Mismatches: 14  
 Query Match: 29.10% Indels: 3  
 DB: 1 Gaps: 1

US-09-194-164-13 (1-918) x HV3G\_HUMAN (1-122)

QY 478 CAGGTGACGCTGTGAGTCTGTGGGGAGCGCTGCTCAGCTGGAGGTCTCTGAGACTG 537  
 |||:::|||||  
 DB 1 GlnValIgluLeuValIgluSerGlyGlyValVal\*\*ProGlyArgSerLeuArgLeu 20  
 |||:::|||||

QY 538 TCCTGTGACGCTGTGATTCCTCCCTCAGAGCTTGTATGACATGCGGTCCGCGAGGCT 597  
 |||:::|||||  
 DB 21 SerCyAlaAlaSerGlyPheThrPheSerAsnTyrAlaMetHisIleTyrValArgGlnPro 40  
 |||:::|||||

QY 598 CTAGGCAAGGGGCTGAGTGGGTGGGAGCTTATATCATATGATGAGAGCACTAATAACTAC 657  
 |||:::|||||  
 DB 41 ProGlyLysGlyLeuGlnTyrValAlaValIleSerTyr\*\*\*Gly\*\*\*\*\*LysTyrTyr 60  
 |||:::|||||

QY 658 GAGAGCTCCGTGAAGGCGGATTCACCATCTCCAGAGACACTCCCAAGACCGGTGAT 717  
 |||:::|||||  
 DB 61 Ala\*\*SerValLysGlyArgPheThrIleSerArgAsp\*\*SerLys\*\*ThrLeuTyr 80  
 |||:::|||||

QY 718 CTAAATAATGACAGCTGAGAACTGAGACAGCGGCTGTATATTACTGTGCGAGAGATCG 777  
 |||:::|||||  
 DB 81 LeuGlnMetAsnSerLeuArgAlaGlu\*\*\*ThrAlaValTyrTyrCysAlaArgAspArg 100  
 |||:::|||||

QY 778 AGCCTGTGGGTGACTATGACCACTACGAGTGTGAGCGTGGGCAAGGGAGCAACG 837  
 |||:::|||||  
 DB 101 ProLeuTyrGly\*\*TyrArgAlaPhe-----AsnTyrTyrGlyGlnGlyThrLeu 117  
 |||:::|||||

QY 838 GTACCCGTCTCTCA 852  
 |||:::|||||  
 DB 118 ValThrValSerSer 122  
 |||:::|||||

RESULT 15  
 Q9UL86 PRELIMINARY; PRT; 109 AA.

AC Q9UL86;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin kappa chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035028; AAD56264.1; -.  
 DR PIR; I30601; I30601.  
 DR HSP; P01625; ILEK3.

DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; IG\_LV.  
 DR SMART: SM00406; IGV: 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 FT MOD RES 1 109  
 FT NON\_TER 1 109  
 SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DNC83 CRC64;

Alignment Scores:  
 Pred. No.: 1.59e-29 Length: 109  
 Score: 497.00 Matches: 99  
 Percent Similarity: 91.15% Conservative: 4  
 Best Local Similarity: 87.61% Mismatches: 6  
 Query Match: 29.01% Indels: 4  
 DB: 2 Gaps: 1

US-09-194-164-13 (1-918) x Q9UL86 (1-109)

QY 70 GATATGTTGAGGACGCTCCAGGACCGCTGTCTTGTCTCAGGGGAAAGACCAAC 129  
 |||:::|||||  
 DB 1 GlnIleValIleuThrGlnSerProGlyThrLeuSerLeuPheProGlyGlnArgAlaThr 20  
 |||:::|||||

QY 130 CTCTCTGCAAGGCGCAGTCAAGAGTGTAGTACAGCTACTTAGCTGTGACCAAGAA 189  
 |||:::|||||  
 DB 21 LeuSerCyAlaArgAlaSerGlnSerValSerSerTyrIleAlaIleTyrGlnGlnLys 40  
 |||:::|||||

QY 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGTGTCATCCACAGGCGCACTGGCATGCCA 249  
 |||:::|||||  
 DB 41 ProGlyGlnAlaProArgLeuLeuIleTyrGlyThrSerSerArgAlaThrGlyLeuPro 60  
 |||:::|||||

QY 250 GACAGGTCAGGCGAGGCGGGTCCGGAGCAGACTTCACTTCACATGATAGTAGTCGAG 309  
 |||:::|||||  
 DB 61 AspArgPheSerGlySerGlySerGluThrAspPheThrIleSerArgLeuGln 80  
 |||:::|||||

QY 310 CCTGAAGATTTCAGTGTATTAATCTGTGACAGAGTATGTAGTCACTTCAGACACTCAG 369  
 |||:::|||||  
 DB 81 ProGlnAspPheAlaValIleTyrTyrCysGlnGlnTyrGlySerSer-----Ile 96  
 |||:::|||||

QY 370 ATCACTTTCGGCGAGGAGCAAGGTGAGATCAAAACA 408  
 |||:::|||||  
 DB 97 PheThrPheGlyProGlyThrIysValAspIleLysArg 109  
 |||:::|||||

Search completed: February 18, 2005, 08:45:55  
 UOB time : 114 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 18, 2005, 06:09:18 ; Search time 94.5 Seconds

(without alignments)  
7514.202 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 1713  
Sequence: 1 GAATTCATGAAAAAACCCG.....ATCACATTAGTAAGCTT 918

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODE=frame+12p\_model -DEV=xlh  
-O=/cgn2\_1/USPRO\_epool/US09194164/runat\_16022005\_122612\_6012/app\_query.fasta\_1.1095  
-DB=GeneSeq\_16Dec04 -QEMT=faaean -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTPMT=pct -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09194164 @CGN\_1\_1\_101 @runat\_16022005\_122612\_6012 -NCPU=6 -ICPU=3  
-DEV MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXt=7

Database: A\_GeneSeq\_16Dec04:\*

1: geneseqp1980s:\*\n2: geneseqp1990s:\*\n3: geneseqp2000s:\*\n4: geneseqp2001s:\*\n5: geneseqp2002s:\*\n6: geneseqp2003as:\*\n7: geneseqp2003bs:\*\n8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1573	91.8	304	2	AAW40070 Human H11
2	1573	91.8	304	2	AAE00947 Human mon
3	1573	91.8	304	7	ABU10486 C-antigen
4	1573	91.8	304	8	ADO52296 Human ant
5	1451.5	84.7	287	2	AAW40071 Human H11
6	1451.5	84.7	287	4	AAE00948 Human mon
7	1451.5	84.7	287	7	ABU10487 C-antigen
8	1451.5	84.7	287	8	ADO52299 Human ant
9	1016.5	59.3	638	6	ADA89103 Phage dis
10	1016.5	59.3	638	6	ADA90139 Anti-Abet

11	1016.5	59.3	638	6	ADA91410 Anti-Abet
12	1016.5	59.3	747	7	ADG74355 MSPRO 11g
13	986	57.6	523	3	AAV44994 HD708CFV-
14	986	57.6	524	3	AAV44995 HD708CFV-
15	972.5	56.8	628	6	ABJ38670 Fab expre
16	961.5	56.1	252	8	AD058062 S2 cell d
17	928	54.2	352	2	AAV06272 Anti-Fc g
18	916.5	53.5	295	5	ABG68848 C219cFv
19	914	53.4	490	3	AAV56637 hCAT1 Bln
20	892	52.1	283	5	AAU75160 Kabat con
21	892	52.1	283	5	ABG73148 Kabat con
22	892	52.1	283	5	ABG73868 Kabat con
23	891.5	52.0	319	5	ABG68851 Interfero
24	887	51.8	263	2	AAW97889 Kabat con
25	866.5	50.6	630	7	ADG69023 Chloropia
26	866.5	50.6	639	7	ADG68991 Chloropia
27	865	50.5	354	3	AAV82515 Anti-HA P
28	863.5	50.4	277	7	ADG69018 Human chl
29	858.5	50.1	250	8	AD161980 Human bcf
30	857.5	50.1	279	7	ABR61568 HIV-1 neu
31	849.5	49.6	252	8	AD040405 Single ch
32	849.5	49.6	252	8	AD040409 Single ch
33	849.5	49.6	253	8	AD040406 Single ch
34	849.5	49.6	254	8	AD040412 Single ch
35	847	49.4	239	8	AD040413 Single ch
36	846.5	49.4	484	6	ABR55341 Amino act
37	840	49.0	247	7	ADG03132 Colon spe
38	834.5	48.7	254	8	ADG17470 HIV envel
39	828.5	48.4	487	6	ADG17475 HIV envel
40	828	48.3	650	6	ABR62591 Anti-CD7
41	828	48.3	651	6	ABR62590 Anti-CD7
42	824.5	48.1	247	8	AD040408 Single ch
43	824.5	48.1	254	8	ADG17468 HIV envel
44	824	48.1	443	6	ABG76488 Humanised
45	824	48.1	443	6	ABG74240 Chimæeric

## ALIGNMENTS

RESULT 1	AAW40070 standard; protein; 304 AA.
ID	AAW40070
AC	AAW40070;
XX	
DT	29-MAY-1998 (first entry)
XX	
DE	Human H11-scFv construct monomer forming protein.
XX	
KW	H11; monoclonal antibody; Mab; C-antigen; variable region heavy chain;
KW	V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe;
KW	primer; vaccine; gene therapy; glioblastoma; neuroblastoma;
KW	malignant melanoma; adenocarcinoma; small cell lung carcinoma;
KW	single chain variable region; scFv.
XX	
OS	Synthetic.
XX	
XX	Homo sapiens.
XX	
XX	MO9744461-A2.
XX	
XX	27-NOV-1997.
XX	
XX	22-MAY-1997; 97WO-US008962.
XX	
XX	22-MAY-1996; 96US-00657449.
XX	
XX	(NOVO-) NOVOSHARM BIOTECH INC.
XX	
XX	Dan MD, Maiti PK, Kaplan HA;
XX	
XX	WPI; 1998-018515/02.
XX	
XX	N-PSDB; AAV10118.

PT Antigen binding fragment from monoclonal antibody, H11 - allows tumour  
PT specific detection and treatment of neoplasia.  
XX  
PS Claim 5, Page 92-93; 126pp; English.

CC This sentence represents a human H1 monoclonal antibody single chain V  
CC region fragment (H1-8cFv) construct which is capable of forming  
CC monomers. This construct is used to determine the ability of H1-8cFv  
CC antibody fragments to bind specifically to the C-antigen on cancer cells.  
CC Such antigen binding fragments may be used for treating a patient with  
CC neoplasia. It is especially useful in the detection of lymphomas and  
CC leukemias where the tumour cells bearing the C antigen are circulating  
CC in the patients bloodstream. The polynucleotide sequence may be used as a  
CC primer or a probe and the encoded protein may be used in a vaccine or for  
CC gene therapy. The human monoclonal antibody (Mab), designated H1,  
CC specifically recognises cancerous cells. H1 is specific for  
CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,  
CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and  
CC prostate adenocarcinoma  
XX  
XX Sequence 304 Aa;

Alignment Scores:	
Pred. No.:	3.9e-18
Score:	1573.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	91.83%
DB:	2
	Gaps: 0
	Indels: 0
	Mismatches: 0
	Conservative: 304
	Matches: 3020
	Length: 304

US-09-194-164-13 (1-918) x AAW40070 (1-304)

OY		GAATTCATGAAAAAACCAGCTACCGCATCCGAGTGGCACTGGCTGTTCGGTACCGGT	60
Dd		1 GlnPheMetLysLYSThrAlaIleAlaIleAlaValAlaLeuAlaIleActylPheAlaThrVal	20
OY		61 GGCGAGGCCGATATTGTGTGTAAGCAGTCTCCAGGCACCCTGTTGTCTCCAGGAGAA	120
Dd		21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln	40
OY		121 AGAGCCACCCCTTCTCTGCGAGGGCCACTCAGAGTGTAAGNAGCGATACCTTAGGCTGGTAC	180
Dd		41 ArgAlaThrLeuSerLysArgAlaSerGlnSerValSerSerSerLysIleuAlaTrpLys	60
OY		181 CAGCAGAAAACCTGGCCAGGCTCCACAGGCTCCTCATATTAGTGTGCATCCACAGGGCCACT	240
Dd		61 GlnGlnLysProGlyGlnAlaProArgLeuLeuIleTyrGlyAlaSerThrArgAlaThr	80
OY		241 GGCGATGCCAGACAGGTTCAGTGGCAGTGGAGTCCGGACAAGACTTCACTCTCACCATCAGT	300
Dd		81 GlyMetProAspArgPheSerGlySerGlyThrAspPheThrLeuThrIleSer	100
OY		301 AGACTGGAGCCCTGAAGAATTTTGCAGTGATATTACTGTCAGAGATGGTAGCTCACTCCAG	360
Dd		101 ArgLeuGlnProGlnAspPheAlaValIleTyrLysGlnGlnIleArgLysSerProGln	120
OY		361 ACACCTCAGATCACTTTCGGCGGAGGAGCCAAAGTGGAGATCAAACGAACTGGCTGCA	420
Dd		121 ThrProGlnIleThrPheGlyGlyGlyThrLysValGluIleLysArgThrValAlaAla	140
OY		421 CCATCTGTCTCTGGCGGTGGCGGTTCCGAGGTGGTGGATCAGGTGGAGGTGCTCCAG	480
Dd		141 ProSerValSerGlyGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlySerGln	160
OY		481 GTGCAGCTGTGGAGCTCTGGGGGAGGCGTGGTCCAGCTGGGAGATCCCTGAACTCTCC	540
Dd		161 ValGlnLeuValGlnSerGlyGlyGlyValGlnProGlyArgSerLeuArgLeuSer	180
OY		541 TGTGAGCTCTGGAGTTCCCTTCAAAAGCTTGTATGATGACCTGGGTCCGCCAGGCTCTA	600
Dd		181 CysAlaAlaSerGlyPheProPheArgSerPheAlaMetHisIrrPValArgGlnAlaLeu	2000
OY		601 GGCAAGGGCTGAGTGGGTGGCGCATTAATATCATATGATGAAAGCAATAAATCTACGA	660

Db	201	GLYLVSGILYENGLINTPValAlaValIleSerIYrNpGLYSerThrIYrTYrAla	220
Qy	661	GACTCCGTGAAAGGCCGATTCACATCTCCAGAGCACTTCCAAAGAACAGCGTGTATCTA	720
Db	221	AspSerValIYGLYrNpGpThrIleSerIYrGpSerThrSerIYrSAsnThrValTYrLeu	240
Qy	721	AAATGAACAGCGCTAGAACTGAGGACAGCGCGTGTATTACTGTGGAGAGATCAGAGC	780
Db	241	LYMeLeAsnSerIeuNpIYrThrIuNpThrAlaValIYrTYrCYsAlaIYrGpNpIser	260
Qy	781	CTGTGGGTGATATGACCACTACTACGGTTTGACGTCTGGAGCAAGGACCAACGCGTC	840
Db	261	LeuLeuGLYrNpTYrNpIYrGpIYrGlyLeuNpValTYrGLYrGLYrThrThrVal	280
Qy	841	ACCGTCTCTCCAGAGTCGAGCAAAAAGTGAATCTGACGGCAAGAAATCTGAACCATCACCAT	900
Db	281	ThrValSerSerGLYrSerGLIuNpIYrLeuIleSerGLIuNpLeuAsnIYrHisHis	300
Qy	901	CACCAT 906	
Db	301	HisHis 302	

RESULT2	
AAE00947	
ID	AAE00947 standard; protein; 304 AA
XX	
AC	AAE00947;
XX	
DT	04-JUL-2001 (first entry)

04-JUL-2001 (first entry)

Human monoclonal antibody H11-single chain variable region (scFv) #1.

Human, monoclonal antibody; Mab; H11, single chain variable region; scFv, neoplastic disease; melanoma; immunoglobulin Ig4; gene therapy; lymphoma; carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine; neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic; C-antigen; chronic leukaemia; glioma.

**Homo sapiens.**

Key	Location/Qualifiers
Region	144.158 /label= Linker
Misc-difference	302.303 /note= "Encoded by CATTACTGAAG"

US6207153-B1.

27-MAR-200

22-MAY-1997; 97US-00862124.

22-MAY-1996; 96US-00657449

(VIVE-) VIVENTIA BIOTECH INC.

Dan MD, Maiti PK, Kaplan HA;

WPI; 2001-289584/30.

—

recognizes an antigen on neoplastic cells but not on normal cells for use

[illegible]

antibody (Mab) H11-ai[n]g]e chain

variable region (scfv). The H11 light chain variable region is linked to

monomers. The invention relates to human monoclonal antibody (mAb) H1A1 (1-27), a single chain variable (v) region fragment and their

corresponding DNA molecules. H11 antibody is an immunoglobulin of IgM subunits which is specific to C-antigen found specifically on neoplastic cells and not on normal cells. H11 is an antibody obtained from the fusion of peripheral blood lymphocytes of a 64 year old male with a low grade glioma and fused to a human myeloma cell line to produce a hybridoma designated NBGM1/H11. A pharmaceutical composition comprising H11 and its derivatives are useful in the diagnosis, imaging and treatment of neoplastic disease, particularly, melanoma, breast carcinoma, lung carcinoma, ovarian carcinoma, colon carcinoma, gastric carcinoma, prostate carcinoma, lymphoma carcinoma, neuroblastoma, glioma, soft tissue sarcoma, small cell lung carcinoma, prostatic adenocarcinoma, B and T cell lymphomas and chronic leukemias. H11 DNA is also used in vaccines and gene therapy

xx Sequence 304 AA;

#### Alignment Scores:

Pred. No.:	3.9e-118	Length:	304
Score:	1573.00	Matches:	302
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	91.83%	Indels:	0
DB:	4	Gaps:	0

US-09-194-164-13 (1-918) x AAE00947 (1-304)

QY 1 GAATTCATGAAAAAACCCTATTCGCGATGCGAGTTGCACTGGCTTGGCTTACCGTT 60  
 Db 1 GTPMCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20  
 QY 61 GCGGAGCGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 Db 21 AAGGAGGAGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 40  
 QY 121 AGAGCACCCTCTCTCTGCGAGGCGCAGTCAAGTGTAGTACGCTGCTGCTGCTGCTGCTGCT 180  
 Db 41 ArgAlaThrLeuSerCysAlaArgLeuSerGlnSerSerSerSerSerSerSerSerSerSer 60  
 QY 181 CAGCAGAACTGCGCGAGGCTCCAGGCTCTCATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 Db 61 GlnGlnLysProGlnGlnAlaProArgLeuLeuIleTyrGlnAlaSerThrArgAlaThr 80  
 QY 241 GGCATGCGCAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
 Db 81 GlyMetProAspArgPheSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 100  
 QY 301 AGACTGAGCCTGAGATTTTGTGCACTGATTTACTGTGCACTGATTTACTGATTTACTGATTTACT 360  
 Db 101 ArgLeuGlnProGlnAspPheAlaValTyrTyrGlnGlnGlnTyrGlnSerSerProGln 120  
 QY 361 ACACCTCAGATCACTTTGCGCGAGGAGCAAGGTTGAGATCAAGGTTGAGATCAAGGTTGAGATCA 420  
 Db 121 ThrProGlnIleThrPheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140  
 QY 421 CCATCTGCTCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 480  
 Db 141 ProSerValSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 160  
 QY 481 GTGAGCTGCTGAGTCTGCGGAGGCGTGTGCTGCGGAGGCTGCGGAGGCTGCGGAGGCTGCGGAGGCT 540  
 Db 161 ValGlnLeuValGlnSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180  
 QY 541 TGTGAGCCTCTGATTCCTCTTCAAGCTTGTGATGCACTGGGCTCGGCGGCTCTTA 600  
 Db 181 CysAlaAlaSerGlnPheProPheArgSerPheAlaMetIleTyrValArgGlnAlaLeu 200  
 QY 601 GGCAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 660  
 Db 201 GlnLysGlnLeuGlnTyrValAlaValIleSerTyrAspGlnSerThrLysTyrTyrVal 220  
 QY 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGACACTTCCAGAGACACTTCCAGAGACACTTCCAGAG 720  
 Db 221 AspSerValLysGlnArgPheThrIleSerArgAspThrSerLysAsnThrValTyrLeu 240

QY 721 AAATGACAGCCTGAGACTGAGACACGCTGCTATTACTTGCAGAGATCAGAC 780  
 Db 241 LysMetAsnSerLeuArgThrGlnAspThrAlaValTyrTyrCysAlaArgAspGlnSer 260  
 QY 781 CGTTGGGATGATGACACTACTACGCTTGGAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
 Db 261 LeuLeuGlnAspTyrAspThrIleTyrGlnLysAspValTyrGlnLysGlnLysThrThrVal 280  
 QY 841 ACCGTCCTCAGATCCGAAACAAATGATCAGCAGAAAGATCTGAACCATCAGCAT 900  
 Db 281 ThrValSerSerGlnSerGlnGlnLysLeuIleSerGlnGlnAspLeuAsnIleHis 300  
 QY 901 CACCAT 906  
 Db 301 HisHis 302  
 RESULT 3  
 ABU10486  
 ID ABU10486 standard; protein, 304 AA.  
 XX ABU10486;  
 AC 07-AUG-2003 (first entry)  
 DT  
 XX  
 DE C-antigen antibody H11 single chain variable region fragment #1.  
 XX Human; antibody; H11; single chain variable region; gene therapy; scfv;  
 KW neoplasia; tumour; recurrence risk; C-antigen; melanoma; neuroblastoma;  
 KW glioma; soft tissue sarcoma; small cell lung carcinoma; brain cancer;  
 KW C-antigen specific antibody; alphac; cancer; vaccine.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 302..303 /note="Encoded by CATTAAGTGAAG"  
 FT  
 PN US2003021779-A1.  
 XX  
 PD 30-JAN-2003.  
 PF 13-FEB-2001; 2001US-00782397.  
 XX  
 PR 22-MAY-1996; 96US-00657449.  
 PR 22-MAY-1997; 97US-00862124.  
 XX  
 PA (DANM/) DAN M D.  
 PA (MAIT/) MAITI P K.  
 PA (KAPL/) KAPLAN H A.  
 PI Dan MD, Maitei PK, Kaplan HA;  
 XX  
 DR WPI, 2003-456278/43.  
 DR N-PSDB; ACP62168; ACP62169.  
 XX  
 PT Novel antigen binding fragment of monoclonal antibody specific for  
 PT antigen detected on neoplastic cells; useful for diagnosing or treating  
 PT cancer, for manufacturing novel reagents and as diagnostic and imaging  
 PT reagent.  
 XX  
 PS Claim 5; Page 34; 62pp; English.  
 XX  
 CC The invention relates to a polypeptide which is an antigen binding  
 CC fragment of a monoclonal antibody specific for an antigen detected on  
 CC neoplastic cells. The antigen binding fragment (ABF) is useful for  
 CC treating a patient with a neoplasia. The individual has a clinically  
 CC detectable tumour. The method is useful for palliating the neoplasia. The  
 CC method reduces the risk of recurrence of a clinically detectable tumour.  
 CC The antigen binding fragment is labelled with a therapeutic moiety such  
 CC as radioisotopes or immunomodulators. ABF is useful for detecting C-  
 CC antigen in a sample. The polypeptide is useful for diagnosing, localising

CC and/or treating neoplasias, including melanoma, neuroblastoma, glioma,  
 CC soft tissue sarcoma and small cell lung carcinoma. The polypeptide is  
 CC useful for manufacturing novel reagents and for treating and imaging  
 CC brain cancer. AβF is useful as a diagnostic and imaging reagent. The  
 CC composition is useful for eliciting an immune response against neoplasia.  
 CC The polynucleotide is useful in expression systems for the production of  
 CC C-antigen specific antibody, termed H11 or alphac, as hybridisation  
 CC probes to assay for the presence of alphac polynucleotide or related  
 CC sequences in a sample, as primers to effect amplification of desired  
 CC polynucleotides and in pharmaceutical compositions including vaccines and  
 CC for gene therapy. The polynucleotide is also useful for genetically  
 CC altering cells in vivo, thus treating various types of cancer. The  
 CC polypeptide, polynucleotide and the composition are useful for detecting  
 CC or treating cancer, including therapy of cancer and prophylactic care,  
 CC particularly for decreasing the risk of recurrence. The present sequence  
 CC represents the amino acid sequence of the human C-antigen specific  
 CC antibody H11 single chain variable region fragment, scFv, #1

XX  
 SQ Sequence 304 AA;

Alignment Scores:

Pred. No.: 3.9e-118 Length: 304  
 Score: 1573.00 Matches: 302  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 91.83% Indels: 0  
 DB: 7 Gaps: 0

US-09-194-164-13 (1-918) X ABU10486 (1-304)

QY 1 GAATTCATGTAAGAAAAACCGGATCGGATCGAGATGCACTGGGCTGTTCCGTACCGTT 60  
 DB 1 GlnpHeMeLysrThrAlaIleAlaValAlaValAlaValAlaValAlaValAlaVal 20  
 QY 61 GCGCAGGCGGATATGTGTGACGAGCTCCAGGACCGCTGTTCTCCAGGAGAA 120  
 DB 21 AAGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln 40  
 QY 121 AAGAGCCACCTCTCCCTGCGAGGCGGACGATCGAGTGTAGTACGCTTACCTGTAC 180  
 DB 41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerYrLeuAlaTrpYr 60  
 QY 181 CAGCAGAAACCTGCGGAGGCTCCAGGCTCCATCATGTGATGATCCAGGCGGACAT 240  
 DB 61 GlnGlnIleProGlyAlaIleAlaProAlaGlnLeuIleYrGlyAlaSerThrAlaTr 80  
 QY 241 GGCATCCAGACAGGTTGATGAGTGGAGTGGTCCGGAACAAGACTTCACTCCACATCA 300  
 DB 81 GlyMetProAspArgPheSerGlySerGlyThrAspPheThrLeuThrIleSer 100  
 QY 301 AAGACTGAGACCTGGAATTTTGGAGTGTATTAATGTCACAGTATGTAGCTCACTCG 360  
 DB 101 ArgGlnIleProGlnAspPheAlaValYrYrCysGlnGlnIleYrGlySerSerProGln 120  
 QY 361 ACACTCAGATCACTTTCGCGGAGGAGCAACAAGTGAAGATCAACAAGACTGTGCTGCA 420  
 DB 121 ThrProGlnIleThrPheGlyGlyGlyThrIleValGlnIleYrArgThrValAlaAla 140  
 QY 421 CCATCTGTCTTGGCGGTGGCGGTTCGGAAGTGTGATCAGTGAAGTGGCTCCAG 480  
 DB 141 ProSerValSerClyGlyGlyGlySerGlyGlyGlySerClyGlyGlyGlySerGln 160  
 QY 481 GTCGACCTGTGAGTGTGCGGAGGCGGTGTCACCTGGAGGCTCCCTGAGACTCTCC 540  
 DB 161 ValGlnLeuValGlnSerGlyGlyGlyValGlnProGlyArgSerLeuArgLeuSer 180  
 QY 541 TGTGACGCTTGATTCCTTCAGAACTTGTATGATCACTGGGTCCGCAAGGCTCA 600  
 DB 181 CysAlaAlaSerClyPheProPheArgSerPheAlaMetHisTrpValArgGlnAlaVal 200  
 QY 601 GGCAGAGGCTGAGTGTGCGGAGTGTATCATATGATGAGAACCTAAATATCATACGA 660  
 DB 201 GlyIleGlyLeuGlnIleProValAlaValIleSerYrAspGlySerThrIleYrYrAla 220

QY 661 GACTCCGTGAGAGGCGCGATTCACCATCTTCAGAGACACTTCCAGAAACAGGTATCTA 720  
 DB 221 AspSerValIleYrGlyArgPheThrIleSerArgAspTrpSerYrAsnThrValYrLeu 240  
 QY 721 AAAAAGAACAGCCTGAGAACTGAGACACGCGTGTCTTACTGTGCGAGATCAGAGC 780  
 DB 241 LysMetLeuSerLeuArgThrGlnAspThrAlaValIleYrYrCysAlaArgAspIleSer 260  
 QY 781 CTGTTGGGTGACTATGACCACTACTACGCTTTTGAACGTCTGGGCGCAAGGACACGCTC 840  
 DB 261 LeuLeuGlyAspYrAspHisIleYrYrGlyLeuAspValTrpGlyIleYrThrVal 280  
 QY 841 ACCGCTCTCTCAGGATCCGGAACAAACTGATCGAGCGGAAGATCTGAACCATGACAT 900  
 DB 281 ThrValSerSerGlySerGlnGlnIleLeuSerGlnGlnAspLeuAsnHisHis 300  
 QY 901 CACCAT 906  
 DB 301 HisHis 302

RESULT 4  
 ADO52296  
 ID ADO52296 standard; protein; 304 AA.  
 XX  
 AC ADO52296;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human antibody H11 scFv protein #1.  
 XX  
 KW Antigen binding fragment; H chain V region; L chain V region; C-antigen;  
 KW neoplasia; cancer; vaccine; gene therapy; human;  
 KW single chain V region fragment; scFv.  
 OS Homo sapiens.  
 XX  
 FT Key location/Qualifiers  
 FT Misc-difference 302..303  
 FT /note="Encoded by CATTCGTGAAG"

US2004091484-A1.  
 PD 13-MAY-2004.  
 XX  
 PF 29-AUG-2003; 2003US-00651453.  
 XX  
 PR 22-MAY-1996; 96US-00657449.  
 PR 22-MAY-1997; 97US-00862124.  
 PR 13-FEB-2001; 2001US-00782397.  
 XX  
 PA (DANM/) DAN M D.  
 PA (MAIT/) MAITI P K.  
 PA (KAPL/) KAPLAN H A.  
 PA (GRAD/) GRAD C.  
 XX  
 PI Dan MD, Maitei PK, Kaplan HA, Grad C;  
 XX  
 DR WPI; 2004-399136/37.  
 DR N-PSDB; ADO52295.  
 XX  
 PT Composition useful for treating neoplasia in patient, comprises antigen  
 PT binding fragment of antibody specifically recognizing C-antigen  
 PT recognized by antibody comprising H chain V region and L chain V region.  
 XX  
 PS Claim 5; SEQ ID NO 14; 56bp; English.

The invention relates to a composition comprising an antigen binding  
 fragment of an antibody comprising H chain V region and L chain V region  
 CC that specifically recognises C-antigen. The invention is useful for  
 CC treating a patient with a neoplasia. The antigen binding fragment of the  
 CC antibody is used as diagnostic and imaging reagents. The invention is  
 CC useful for genetically altering cells in vivo, to treat various types of



CC cancer. It is also useful in vaccine and gene therapy. The present  
 CC sequence is human antibody H11 single chain V region fragment (scfv).  
 XX  
 SQ Sequence 304 AA;

Alignment Scores:  
 Pred. No.: 3.9e-118 Length: 304  
 Score: 1573.00 Matches: 302  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 91.83% Indels: 0  
 DB: 8 Gaps: 0

US-09-194-164-13 (1-918) x ADO52296 (1-304)

```

QY 1 GAATTCATGAAAAAACCCTATCGCGATCGAGTTGCACTGGCTGGTTTCCTACCGTT 60
DB 1 GluphmetelylyethrthralalelaialaValaleuhalaglyphealathrVal 20
QY 61 GGGCAGCCGATATTGTTGACGGCAGTCTCCAGGACCCCTGTTTCTCCAGGGGAA 120
DB 21 AAlaGlnAlaAspIleValleuthrGlnSerProGlyThrLeuSerLeuSerProGlyGln 40
QY 121 AGAGCCACCTCTCTCGACAGGGCCAGTCAAGTGTAGTAGAGCTTAAAGCTGTAC 180
DB 41 ArgAlaThrLeuSerGlyArgAlaSerGlnSerValSerSerSerThrLeuAlaIlePyr 60
QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTATGTCATCCACAGGCGACT 240
DB 61 GInGlnIlyProGlyIyAlaIleProAlaGluLeuIleTyrGlyAlaSerThrArgAlaThr 80
QY 241 GGCATGCCAGACAGATTGACAGTGGCTGGGACAGACTTCACTCAGCATCACT 300
DB 81 GlyMetProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer 100
QY 301 AGACTGAGACCTGAAAGATTGTCAGTGTATTACTGTCAGACAGATGTAGTCACTCCAG 360
DB 101 ArgLeuGluProGluIleAspPheAlaValIlyTyrCysGlnGlnIlyIySerSerProGln 120
QY 361 ACACTTCAGATCACTTTCGCGAGGAGGACCAAGGTGAGATCAAAAGAACTGTGGCTGCA 420
DB 121 ThrProGlnIleThrPheGlyIyGlyIyThrIyValGlnIleValArgThrValAlaIle 140
QY 421 CCATCTGTCTTCGCGGCTGGCGGTTCCGAGGTGTGATCAAGGTGAGAGTGGCTCCAG 480
DB 141 ProSerValSerGlyIyGlyIySerGlyIyGlyIySerGlyIyGlyIySerGln 160
QY 481 GTGCACTGTGAGAGTCTGGGAGGCGATGTCAGGCTGGGAGGCTCCAGACTCTCC 540
DB 161 ValGlnLeuValGlnSerGlyIyGlyIyValIyValGlnProGlyArgSerLeuArgLeuSer 180
QY 541 TGTGCAAGCTCTGATTCCTCTTCAGAACTTGTCTATGCACTGGTCCGCGAGGCTCTTA 600
DB 181 CysAlaIleAspSerGlyPheProPheArgSerPheAlaMetIleThrValArgGlnAlaLeu 200
QY 601 GCGAAGGGGCTGAGTGGGTGGGAGTTATATCATATGATGAAAGCACTAAATACTACGA 660
DB 201 GlyIySerGlyLeuGlnIlyThrValAlaValIleSerIyAspGlySerThrIySerIyAla 220
QY 661 GACTCGGAAAGGGCCGATTCACTTCAGAGCACTTCCAGAAAGCGGTATCTCA 720
DB 221 AspSerValIyGlyIyArgPheThrIleSerArgAspThrSerIyAspThrValIyIyLeu 240
QY 721 AAATGAACAGCCTGAGAACTGAGGACAGCGCTGTCTATTACTGTGCGAGATCAGAC 780
DB 241 IyMetAsnSerIleuArgThrGlnAspThrAlaValIyTyrCysAlaArgAspGlnSer 260
QY 781 CTGTTGGGAGACTATGACCACTACACGTTTGGACGTTGGGGCAAGGAGCACAGGTC 840
DB 261 IeuLeuGlyAspIyAspIyArgPheIyTyrGlyLeuAspValIyThrGlyIyThrVal 280
QY 841 ACCGTCCTCGTCAAGATCCGAACAAAACTGATCAGGAGAGAAAGATCTGAACATCAACCT 900

```

DB 281 ThrValSerSerGlySerGlnIyLeuIleSerGlnIyAspLeuAsnHisHis 300  
 QY 901 CACCAT 906  
 DB 301 HisHis 302

RESULT 5  
 AAM40071  
 ID AAM40071 standard; protein, 287 AA.  
 AC AAM40071;  
 XX  
 DT 29-MAY-1998 (first entry)

XX Human H11-scFv construct dimer forming protein.  
 DE  
 XX H11; monoclonal antibody; Mab; C-antigen; variable region heavy chain;  
 KW V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe;  
 KW primer; vaccine; gene therapy; glioblastoma; neuroblastoma;  
 KW malignant melanoma; adenocarcinoma; small cell lung carcinoma;  
 KW single chain variable region; scFv.

OS Synthetic.  
 OS Homo sapiens.

PN WO9744461-A2.

PD 27-NOV-1997.

PP 22-MAY-1997; 97WO-US008962.

PK 22-MAY-1996; 96US-00657449.

PA (NOVO-) NOVOPHARM BIOTECH INC.

PI Dan MD, Maitl PK, Kaplan HA;

DR WPI, 1998-018515/02.

DR N-PSDB; AAV10119.

PT Antigen binding fragment from monoclonal antibody, H11 - allows tumour  
 PR specific detection and treatment of neoplasia.  
 PS Claim 5; Page 95-96; 126pp; English.

XX This sequence represents a human H11 monoclonal antibody single chain V  
 CC region fragment (H11-scFv) construct which is capable of forming dimers.  
 CC This construct is used to determine the ability of H11-scFv antibody  
 CC fragments to bind specifically to the C-antigen on cancer cells. Such  
 CC antigen binding fragments may be used for treating a patient with  
 CC neoplasia. It is especially useful in the detection of lymphomas and  
 CC leukaemias where the tumour cells bearing the C antigen are circulating  
 CC in the patients bloodstream. The polynucleotide sequence may be used as a  
 CC primer or a probe and the encoded protein may be used in a vaccine or for  
 CC gene therapy. The human monoclonal antibody (Mab), designated H11,  
 CC specifically recognises cancerous cells. H11 is specific for  
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,  
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and  
 CC prostate adenocarcinoma

SQ Sequence 287 AA;

Alignment Scores:

Pred. No.: 2.38e-108 Length: 287  
 Score: 1451.50 Matches: 283  
 Percent Similarity: 93.71% Conservative: 0  
 Best Local Similarity: 93.71% Mismatches: 2  
 Query Match: 84.73% Indels: 17  
 DB: 2 Gaps: 1

US-09-194-164-13 (1-918) x AAM40071 (1-287)

```

QY 1 GAATTCATGAAAAAACCCTATCGCGATCGAGTTGCACTGGCTGGTTTCCTACCGTT 60

```



```

Db      41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerTyrluAlaTrpTyr 60
QY      181 CAGCAAGAAACCTGGCGAGGCTCCGAGGCTCCATCTATATGATGATCCAGCGGCACT 240
Db      61 GlnGlnLysProGlyGlnAlaProArgLeuLeuIleTyrglyAlaSerThrArgAlaThr 80
QY      241 GGCATGCCAGACAGGATTCAGTGGAGGGATCCGGGACAGACTTCACCTCACTCACT 300
Db      81 GlyMetProAspArgPheSerSerGlySerGlySerGlyThrAspPheThrIleSer 100
QY      301 AGACTGAGACCTGAAAGATTTCAGTGTATTACTGTACAGCACTATGATGATGATGAT 360
Db      101 ArgLeuGlnLysProGlyLysPheAlaValTyrTyrCysGlnGlnTyrGlySerSerProGln 120
QY      361 ACACCTCAGATCACTTTCGGCGGAGGAGCAAGAGTGGAGATCAAAAGCACTGGCTGCA 420
Db      121 ThrProGlnIleThrPheGlyGlyGlyThrLysValGlnIleLysArgThrValAlaAla 140
QY      421 CCATCTGTCTCTGGCGGTGGCGGTTCCGGAGGTGTGATCAGTGGAGGTGGCTCCCA 480
Db      141 -----SerGlyGln 143
QY      481 GTGCAAGCTGTGAGATCTGGGGAGGCGGTGTCCAGCCTGGAGGCTCCCTGAGACTCTCC 540
Db      144 ValGlnLeuValGlnSerGlyGlyGlyValGlnProGlyArgSerLeuArgLeuSer 163
QY      541 TGTGAGGCTCTGAGATTCCTTCAGAAAGCTTTCATATGATGATGATGATGATGATGAT 600
Db      164 CysAlaAlaSerGlyPheProPheArgSerPheAlaMetIleTrpValArgGlnAlaLeu 183
QY      601 GCGAAGGGGCTGTGAGTGGGTGGAGTATATCATATGATGATGATGATGATGATGATGAT 660
Db      184 GlyLysGlyLeuGlnIleTrpValAlaValIleSerTyraAspGlySerThrLysTyraAla 203
QY      661 GACTCCGTGAAGGCGCATTCACATCTCCAGAGACACTTCCAGAAACGCGTGTATCTTA 720
Db      204 AspSerValLysGlyArgPheThrIleSerArgAspThrSerLysAsnThrValTyrLeu 223
QY      721 AAAATGAACAGCTGAGAACTGAGACACACGCGTGTCTATTACTGTGCGAGAGATCAAGC 780
Db      224 LysMetAsnSerLeuArgThrGlnAspThrAlaValTyrTyrCysAlaArgAspGlnSer 243
QY      781 CTGTGGGAGTACTAGACCACTACACTACAGCTTGGAGTGGGAGGAGGAGCAACGCTGC 840
Db      244 LeuLeuGlyAspTyrAspHisTyrTyrGlyLeuAspValTrpGlyLysGlyThrTrpVal 263
QY      841 ACCGTCTCTCAGATCCGAAACAAATGATCAGCGAAGAGATCTGACCATCAGCAT 900
Db      264 ThrValSerSerGlySerGlnGlnIleLeuIleSerGlnGlnLysAspLeuAsnHisHis 283
QY      901 CACCAT 906
Db      284 HisHis 285

```

RESULT 7  
ABU10487 standard; protein; 287 AA.

XX ABU10487;  
XX AC  
XX DT 07-AUG-2003 (first entry)  
XX DE C-antigen antibody H11 single chain variable region fragment #2.  
XX EE  
XX FF Human; antibody; H11; single chain variable region; gene therapy; scFv;  
XX GG neoplasia; tumour; recurrence risk; C-antigen; melanoma; neuroblastoma;  
XX HH glioma; soft tissue sarcoma; small cell lung carcinoma; brain cancer;  
XX II C-antigen specific antibody; alphac; cancer; vaccine.  
XX JJ Homo sapiens.  
XX KK Synthetic.  
XX LL  
XX MM Key Location/Qualifiers

```

FT      Misc-difference 285..286
FT      /note= "Encoded by CATTAGTGAAG"
XX      US2003021779-A1.
XX      30-JAN-2003.
XX      13-FEB-2001; 2001US-00782397.
XX      22-MAY-1996; 96US-00657449.
XX      PR 22-MAY-1997; 97US-00862124.
XX      PA (DANM/) DAN M D.
XX      PA (MATI/) MATI P K.
XX      PA (KAPL/) KAPLAN H A.
XX      PI Dan MD, Maiti PK, Kaplan HA;
XX      WPI: 2003-456278/43.
XX      DR N-PsDB; ACA62170, ACA62171.
XX      PT Novel antigen binding fragment of monoclonal antibody specific for
XX      PT antigen detected on neoplastic cells, useful for diagnosing or treating
XX      PT cancer, for manufacturing novel reagents and as diagnostic and imaging
XX      PT reagent.
XX      Claim 5; Page 36-37; 62pp; English.
XX      The invention relates to a polypeptide which is an antigen binding
XX      CC fragment of a monoclonal antibody specific for an antigen detected on
XX      CC neoplastic cells. The antigen binding fragment (ABF) is useful for
XX      CC treating a patient with a neoplasia. The individual has a clinically
XX      CC detectable tumour. The method is useful for palliating the neoplasia. The
XX      CC method reduces the risk of recurrence of a clinically detectable tumour.
XX      CC The antigen binding fragment is labelled with a therapeutic moiety such
XX      CC as radioisotopes or immunomodulators. ABF is useful for detecting C-
XX      CC antigen in a sample. The polypeptide is useful for diagnosing, localising
XX      CC and/or treating neoplasias, including melanoma, neuroblastoma, glioma,
XX      CC soft tissue sarcoma and small cell lung carcinoma. The polypeptide is
XX      CC useful for manufacturing novel reagents and for treating and imaging
XX      CC brain cancer. ABF is useful as a diagnostic and imaging reagent. The
XX      CC composition is useful for eliciting an immune response against neoplasia.
XX      CC The polynucleotide is useful in expression systems for the production of
XX      CC C-antigen specific antibody, termed H11 or alphac, as hybridisation
XX      CC probes to assay for the presence of alphac polynucleotide or related
XX      CC sequences in a sample, as primers to effect amplification of desired
XX      CC polynucleotides and in pharmaceutical compositions including vaccines and
XX      CC for gene therapy. The polynucleotide is also useful for genetically
XX      CC altering cells in vivo, thus treating various types of cancer. The
XX      CC polypeptide, polynucleotide and the composition are useful for detecting
XX      CC or treating cancer, including therapy of cancer and prophylactic care,
XX      CC particularly for decreasing the risk of recurrence. The present sequence
XX      CC represents the amino acid sequence of the human C-antigen specific
XX      CC antibody H11 single chain variable region fragment, scFv, #2
XX      SQ Sequence 287 AA;

```

Alignment Scores:

Pred. No.:	2,38e-108	Length:	287
Score:	1451.50	Matches:	283
Percent Similarity:	93.71%	Conservative:	0
Best Local Similarity:	93.71%	Mismatches:	2
Query Match:	84.73%	Indels:	17
DB:	7	Gaps:	1

US-09-194-164-13 (1-918) x ABU10487 (1-287)

```

QY      1 GAATTCATGAAAGAAACCGCTATCGCGATCCGATGTCATGCTGCTTGCCTACCGTT 60
Db      1 GlnPheMetLysLysThrAlaIleAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrVal 20
QY      61 GCGCAGGCGGATGATGTTGTGACGAGTCTCCAGGACCCCTGCTTGTCTCCAGGGGAA 120

```

```

Db      21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln 40
QY      121 AGAGCCACCTCTCTGCGAGGGCCAGTCAGAGTGTATAGACGACTTACCTGGTAC 180
Db      41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerTyLeuAlaTrpTyr 60
QY      181 CAGCAGAAACCTGGCGAGGCTCCCGAGGCTCCATCTATAGTGACATCCACGAGGCACT 240
Db      61 GlnGlnLysProGlyGlnAlaProArgLeuLeuIleTyGlyAlaSerThrArgAlaThr 80
QY      241 GGCATGCCAGACAGGTTCAGTGAGGAGTCCGGAGCAGACTTCACTTCACATCACT 300
Db      81 GlyMetProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer 100
QY      301 AGACTGAGACCTGGAAGATTTTGAGTGTATTACTGTCAAGATTAAGTACCTTCAG 360
Db      101 ArgLeuGlnLysProGlyLysPheAlaValTyrCysGlnGlnIleTyGlySerSerProGln 120
QY      361 AGACCTCAGATCACTTTGGCGAGGAGCAAGAGTGGAGATCAAAAGCACTGGCTGCA 420
Db      121 ThrProGlnIleThrPheGlyGlyGlyTyrTrpValGlnIleLysArgThrValAlaAla 140
QY      421 CCATCTGTCTCGCGGTGGCGGTTCCGAGGTGTGATCAGATGAGTGGCTCCAG 480
Db      141 -----serGlyGln 143
QY      481 GTGCAAGCTGTGAGTCTGGGGAGGCGGTGTCCAGCTGGAGGTCCTGAGACTTCC 540
Db      144 ValGlnLeuValGlnSerGlyGlyGlyValGlnProGlyArgSerLeuArgLeuSer 163
QY      541 TGTGCAAGCTGTGAGTCTCCCTTCAAGACTTGTGATCAGCTGGGTCCGCGAGGCTCA 600
Db      164 CysAlaAlaSerGlyPheProPheArgSerPheAlaMetIleTrpAlaArgGlnAlaLeu 183
QY      601 GCGAAGGGGCTGAGTGGTGGCAGTATATATATATATATATATATATATATATATATAT 660
Db      184 GlyLysGlyLeuGlnTrpValAlaValIleSerTyArgGlySerThrIleTyTrpAla 203
QY      661 GACTCCGTGAGAGGCGGATTCACCATCTCCAGAGACACTTCCAGAAACCGGTATCTTA 720
Db      204 AspSerValLysGlyArgPheThrIleSerArgAspThrSerLysAsnThrValTyrLeu 223
QY      721 AAAATGAACAGCTGAGACGAGCAGAGCAGGCTGATATATATATATATATATATATAT 780
Db      224 LysMetAsnSerLeuArgThrGlnAspTrpAlaValTyrTyrCysAlaArgAspGlnSer 243
QY      781 CTGTTGGTGAATATGACCACTACTACGCTTGGACGTCGTGGGGCAAGAGCAACGCTC 840
Db      244 LeuLeuGlyAspTrpAspHisIleTyTrpGlyLeuAspValTrpGlyLysGlyThrVal 263
QY      841 ACCGTCCTCTCAGATCCGAAACAAAACCTGATCAGCGAAGAAAGATCTGAACCATCC 900
Db      264 ThrValSerSerGlySerGlnGlnLysLeuIleSerGlyLysAspLeuAsnHisIleHis 283
QY      901 CACCAT 906
Db      284 HisHis 285

```

```

XX      XX      Key      Location/Qualifiers
FH      FH      MISC-difference 285..286
FT      FT      /note="Encoded by CARTGTGAAAG"
PN      PN      US2004091484-A1.
XX      XX      13-MAY-2004.
PD      PD      29-AUG-2003; 2003US-00651453.
XX      XX      22-MAY-1996; 96US-00657449.
PR      PR      22-MAY-1997; 97US-00862124.
PR      PR      13-FEB-2001; 2001US-00782397.
XX      XX      (DANM/) DAN M. D.
PA      PA      (MATT/) MATTI P. K.
PA      PA      (KAPL/) KAPLAN H. A.
PA      PA      (GRAD/) GRAD C.
PI      PI      Dan MD, Matti PK, Kaplan HA, Grad C;
XX      XX      WPI; 2004-399136/37.
DR      DR      N-PSDB; ADO52298.
XX      XX      Composition useful for treating neoplasia in patient, comprises antigen
PT      PT      binding fragment of antibody specifically recognizing C-antigen
PT      PT      recognized by antibody comprising H chain V region and L chain V region.
PS      PS      Claim 5; SEQ ID NO 17; 56bp; English.
XX      XX      The invention relates to a composition comprising an antigen binding
CC      CC      fragment of an antibody comprising H chain V region and L chain V region
CC      CC      that specifically recognises C-antigen. The invention is useful for
CC      CC      treating a patient with a neoplasia. The antigen binding fragment of the
CC      CC      antibody is used as diagnostic and imaging reagents. The invention is
CC      CC      useful for genetically altering cells in vivo, to treat various types of
CC      CC      cancer. It is also useful in vaccine and gene therapy. The present
CC      CC      sequence is human antibody H11 single chain V region fragment (scFv).
XX      XX      SQ      Sequence 287 AA;
XX      XX      Alignment Scores:
Pred. No.: 2,386-108 Length: 287
Score: 1451.50 Matches: 283
Percent Similarity: 93.71% Conservative: 0
Best Local Similarity: 93.71% Mismatches: 2
Query Match: 84.73% Indels: 17
DB: 8 Gaps: 1
US-09-194-164-13 (1-918) x ADO52299 (1-287)
QY      1 GAATTCATGAAAAAACCAGCTATCCGATCGCAGTTGCACTGGCTGGTTGCTACCGTT 60
Db      1 GiuphMeTyLysThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrVal 20
QY      61 GGCAGAGCCGATATGTTGTCAGCGAGCTCCAGGACCCGTCTTGTCTCCAGGGGAA 120
Db      21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln 40
QY      121 AGAGCCACCTCTCTGCGAGGGCCAGTCAGAGTGTATAGACGACTTACCTGGTAC 180
Db      41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerTyLeuAlaTrpTyr 60
QY      181 CAGCAGAAACCTGGCGAGGCTCCCGAGGCTCCATCTATAGTGACATCCACGAGGCACT 240
Db      61 GlnGlnLysProGlyGlnAlaProArgLeuLeuIleTyGlyAlaSerThrArgAlaThr 80
QY      241 GGCATGCCAGACAGGTTCAGTGAGGAGTCCGGAGCAGACTTCACTTCACATCACT 300
Db      81 GlyMetProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer 100
QY      301 AGACTGAGACCTGGAAGATTTTGAGTGTATTACTGTCAAGATTAAGTACCTTCAG 360

```

```

DB      101  ArgLeuGluProGluAspPheAlaValTyrTrpCysGlnGlnTyrCysSerSerProGln 120
QY      361  ACACCTCAGATCACTTTGGCGGAGGACCAAGGTGGAGATCAACGAACTGTGGCTGCA 420
DB      121  ThrProGlnIleThrPheGlyGlyGlyThrLysValGluIleLysArgThrValAlaIle 140
QY      421  CCATCTGTCTCGGGGCGGTGCGGTTCCGAGGTGGATCAAGGTGGAGGTGCTCCGAG 480
DB      141  -----SerGlyGln 143
QY      481  GTGCACTGTGTGAGTCTGGGGAGGCGGTGTCAGCCTGGAGGTCCTGAGACTCTCC 540
DB      144  ValGlnLeuValGlnSerCysGlyValValGlnProGlyArgSerLeuArgLeuSer 163
QY      541  TGTGCAAGCTCTGATTCCTCCCTTCAGAGCTTTGCTATGCACTGGGCTCCGACGCTCTA 600
DB      164  CysAlaAlaSerGlyPheProPheArgSerPheAlaMetHisIleTrpValArgGlnAlaLeu 183
QY      601  GGCAAGGGGCTGAGTGGGTGGCACTTATATCATATGATGGAAGCACTTAAATACCTACGA 660
DB      184  GlyLysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerThrLysTyrTrpAla 203
QY      661  GACTCCGTGAAGGGCGGATTCACCATCTCCAGAGACACTTCCAGAAACAGCGGTATCTTA 720
DB      204  AspSerValLysGlyArgPheThrIleSerArgAspThrSerLysAsnThrValTyrLeu 223
QY      721  AAATGAACAGCGCTGAGAACTGAGGACAGCGGCTCTATTACTGTGCGAGATCAGAGC 780
DB      224  LysMetAsnSerLeuArgThrGlnAspThrAlaValTyrTrpCysAlaArgAspGlnSer 243
QY      781  CTGTGGGTGATATGACCACTACTACTACGTTTGACGTTGGGGGCAAGGGACACCGGTC 840
DB      244  LeuLeuGlyAspTyrAspHisTyrTrpGlyLeuAspValTyrGlyLysGlyThrThrVal 263
QY      841  ACCGTCCTCCAGATCCGACCAAAATGATCAGGAGGAAGATCTGAACATCAGCATCACC 900
DB      264  ThrValSerSerGlySerGlnGlnLysLeuIleSerGlnGlnAspLeuAsnHisHis 283
QY      901  CACCAT 906
DB      284  HisHis 285

```

```

XX      (PROC-) PROCHON BIOTECH LTD.
PA      Yavon A, Rom E;
XX      WPI, 2003-175236/17.
DR      N-PsDB; ADA89102.
XX      New antibodies which have specific binding affinity for a receptor
PT      protein tyrosine kinase (RPTK) and block constitutive activation of RPTK,
PT      useful for treating bone and cartilage disorders, or malignant cell
PT      proliferative diseases.
PS      Example 3; Fig 29B; 122pp; English.
XX      The present invention describes a molecule (I) comprising the antigen
CC      binding portion of an isolated antibody which has specific binding
CC      affinity for a receptor protein tyrosine kinase (RPTK), particularly for
CC      a fibroblast growth factor receptor (FGFR), and which blocks constitutive
CC      activation of an RPTK. Also described: (1) pharmaceutical compositions
CC      comprising (I) as an active ingredient and a pharmaceutical carrier,
CC      excipient, or auxiliary agent; (2) a kit comprising (1), at least one
CC      reagent for detecting the presence of (1) when bound to the RPTK, and
CC      instructions for use; (3) a method for treatment of bone and cartilage
CC      related disorders by administering a composition of (1) to the subject;
CC      (4) a method for treating or inhibiting a cell proliferative disease or
CC      disorder by administering the composition of (1); (5) a method for
CC      screening a molecule comprising the antigen-binding portion of an
CC      antibody which blocks ligand-dependent activation of RPTK; (6) an
CC      isolated nucleic acid molecule encoding a VJ-CDR3 DNA region and a VH-
CC      CDR3 DNA region; (7) an isolated nucleic acid molecule encoding VJ region
CC      and a VH region; (8) vectors comprising a nucleic acid molecule of (6) or
CC      (7); and (9) host cells transformed with the vector. (I) have
CC      osteopapthic, cytoskeletal and ophthalmological activities, and can be used
CC      as a RPTK inhibitor. Compositions comprising (I) are useful for treating
CC      bone and cartilage disorders, including skeletal disorders such as
CC      skeletal dysplasia (achondroplasia, chondroplasia, chondrodysplasia,
CC      hypochondroplasia, severe achondroplasia with developmental delay and
CC      acanthosis nigricans dysplasia) or a craniosynostosis disorder (e.g.
CC      Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis
CC      nigricans). The composition may also be used for treating or inhibiting
CC      malignant cell proliferative disease or disorder associated with abnormal
CC      RPTK activity, including a haematopoietic malignancy (e.g. multiple
CC      myeloma), solid tumours (e.g. mammary, colon, cervical, bladder,
CC      colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary
CC      tumours, tumour progression (particularly progression of transitional
CC      cell carcinoma or mammary carcinoma), or tumour metastasis, where the
CC      cell proliferative disorder may be associated with the action of a
CC      constitutively activated RPTK, or with ligand-dependent activation of
CC      RPTK. The compositions may further be used for treating
CC      hyperproliferative diseases and disorders associated with ligand-
CC      dependent FGFR signaling, such as vision disorders (e.g. neovascular
CC      glaucoma, macular degeneration and proliferative retinopathy including
CC      diabetic retinopathy), and non-neoplastic angiogenic pathological
CC      conditions (e.g. haemangiomas, angiodiomas and psoriasis). The present
CC      sequence is given in the exemplification of the present invention.
XX      SQ      Sequence 638 AA;
XX
XX      Alignment Scores:
XX      Pred. No.:      3e-73
XX      Score:           1016.50
XX      Percent Similarity: 61.86%
XX      Best Local Similarity: 57.99%
XX      Query Match:      59.34%
XX      DB:              6
XX      Gaps:            5
XX
XX      US-09-194-164-13 (1-918) x ADA89103 (1-638)
QY      7  ATGAAAAAACCGCTATCGCATGCGATTCGACTGCGTTCGCTACCGTTGCGAG 66
DB      1  MetLysLysThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrValAlaGln 20

```

```

QY 67 GCGGATATTTGGTTGACAGGAGTCTCCAGGACACCTGTCTTGGTCCAGGGGAAAGGCC 126
DB 21 AlaAspIleValLeuThrGlnSerProAlaThrLeuSerLeuSerProIleGlnArgAla 40
QY 127 ACCCTCTCCGAGGGCCAGTACAGATGTAGTACAGAGCTTACCTGTATCCAGCAG 186
DB 41 ThrLeuSerCysArgAlaSerGlnSerValSerSerSerTyrLeuAlaIlePyrGlnGln 60
QY 187 AAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGTGATCCACAGGGCCACTGGCATG 246
DB 61 LysProGlnIleAlaProArgLeuIleTyrGlnIleValSerSerArgAlaThrGlnVal 80
QY 247 CAGAGAGGTTGAGGGGAGGTCGGGACAGACTTCACTCACTCACTCACTCACTGAGACG 306
DB 81 ProAlaArgPheSerTyrSerGlnSerGlnTyrThrAspPheThrLeuThrIleSerSerLeu 100
QY 307 GAGCCTGAGATTTTGGCAGTGTATTACTGTCCAGCATGATGATGATGATGATGATGATG 366
DB 101 GlnProGlnAspPheAlaValTyrTyrCysGlnGlnIleTyrThrThrProPro----- 118
QY 367 CAGATCACTTTGGCGGAGGAGACCAAGGTGAGATGAAACAACTGTGCTGCACCATCT 426
DB 119 -----ThrPheGlnGlnIleTyrThrValIleGlnIleArgThrValAlaIleProSer 136
QY 427 GTC----- 429
DB 137 ValPheIlePheProProSerAspArgIleGlnLeuLysSerGlyThrAlaSerValValCys 156
QY 429 ----- 429
DB 157 LeuLeuAsnAsnPheTyrProArgIleValIleValGlnThrLysValAlaAspAsnAlaLeu 176
QY 430 ---TCTGGC----- 435
DB 177 GlnSerGlnAsnSerGlnIleSerValIleThrGlnIleAspSerLysAspSerThrTyrSer 196
QY 435 ----- 435
DB 197 LeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlnLysHisLysValIleValCys 216
QY 436 -----GGTGGCGGTTCCGGAGGTGCTGATGATGATGATGATGATGATGATGATGATG 474
DB 217 GluValThrHisGlnIleGlnLeuSerSerProValThrLysSerPheAsnArgIleGlnAla 236
QY 474 ----- 474
DB 237 MetLysGlnSerThrIleAlaLeuAlaLeuLeuProLeuLeuPheThrProValThrLys 256
QY 475 TCCCGAGTGCAGTGTGAGTGTGGGAGGCGGTGTCAGGCTGGGAGGTCCCGTGAAGA 534
DB 257 AlaGlnValGlnLeuValGlnSerGlnGlnIleValGlnProGlnIleGlnSerLeuArg 276
QY 535 CTCTCCCTGTCAGCCTCTGATTTCCCTTCAGAAAGCTTGTCTATGACATGCGGCTCCAG 594
DB 277 LeuSerCysAlaIleSerGlnPheThrPheSerSerTyrAlaMetSerTrpValAlaGln 296
QY 595 GCTTACGGGAGGCGCTGAGTGGGTGGCATTTATTCATTAAGATGGAAGCACTAAATAC 654
DB 297 AlaProGlnLysGlnIleGlnIleTrpValSerAlaIleSerGlnSerGlnIleSerThrTyr 316
QY 655 TACGAGATCCGCTGAAAGGCGGATTCACATTCACAGAGACACTTCGAAGAAGCAGG 714
DB 317 TyrAlaAspSerValLysGlnIleArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 336
QY 715 TATCTAAATGAACAGCTGGAACCTGAGACACGCGCTGTCTATTACTGTGCGAGAGAT 774
DB 337 TyrIleGlnMetAsnSerLeuArgAlaGlnAspThrAlaValIleTyrTyrCysAlaArg---- 355
QY 775 CAGAGCCTGTTGGGTACTATGACCACTACTACGCTTTGAGACCTCGGGGCAAGGGAGCC 834
DB 356 -----TrpIleGlnLysArgGlnPheTyrAlaMetAspArgTrpGlnGlnIleGln 371
QY 835 ACGGTACCGCTCTCCCTCAGAGATCC 858

```

```

DB 372 LeuValThrValSerSerAlaSer 379
RESULT 10
ADA90139
ID ADA90139 standard, protein, 638 AA.
XX
AC ADA90139;
XX
DT 20-NOV-2003 (first entry)
XX
DE Anti-Abeta antibody related amino acid sequence SEQ ID NO:254.
XX
KW antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
KW neurotropic; antiparkinsonian; gene therapy; amyloidogenesis;
KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
KW Alzheimer's disease; motor neuropathy; Down's syndrome;
KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
KW neuronal disorder; aging.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN MO200307060-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-EP001759.
XX
PR 20-FEB-2002; 2002EP-00003844.
XX
PA (HOF) HOFFMANN LA ROCHE & CO AG F.
PA (MORP-) MORPHOSYS AG.
PI Bardoff M, Bohrmann B, Brockhaus M, Huber W, Kretschmar T,
PI Loening C, Loetscher H, Nordstedt C, Rothe C,
XX
DR WPI, 2003-663848/62.
XX
PT New antibody molecule capable of specifically recognising two regions of
PT the beta-A4 peptide, useful for diagnosing, preventing or treating
PT diseases associated with amyloidogenesis or amyloid-plaque formation
PT (e.g. dementia).
XX
PS Disclosure, Page 251-254; 312pp; English.
XX
CC The present invention describes an antibody molecule (I) capable of
CC specifically recognising two regions of the beta-A4 peptide/Abeta4. The
CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
CC Ser-Gly-Tyr AD89886 or its fragment, and the second region comprises the
CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-
CC Gly AD89887 or its fragment. Also described: (1) a nucleic acid molecule
CC encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host
CC cell comprising the vector of (2); (4) preparing (1), comprising
CC culturing the host cell of (3) under conditions that allow synthesis of
CC (1) and recovering (1) from the culture; (5) a composition comprising (1)
CC or an antibody molecule produced by method (4); (6) a kit comprising (1),
CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
CC (1); (8) testing the resulting Fab optimisation library by panning
CC against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing
CC of selected, optimised clones; (11) preparing a pharmaceutical
CC composition, comprising optimisation of (1), and formulating the
CC optimised antibody/antibody molecule with a carrier; and (12) a
CC pharmaceutical composition prepared by method (8). (1) has
CC neuroprotective, neurotropic and antiparkinsonian activities, and can be
CC used in gene therapy. The antibody molecule (I), nucleic acid molecule,
CC vector or host is useful in preparing a pharmaceutical composition for
CC the prevention and/or treatment of a disease associated with
CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule
CC may also be used in preparing a diagnostic composition for the detection
CC of the disease mentioned above. The antibody is used for the
CC disintegration of beta-amyloid plaques or for passive immunisation

```

CC against beta-amyloid plaque formation. In particular, the disease is  
 CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,  
 CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with  
 CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,  
 CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The  
 CC present sequence is used in the exemplification of the present invention.

XX Sequence 638 AA:

Alignment Scores:

Pred. No.:	3e-73	Length:	638
Score:	1016.50	Matches:	225
Percent Similarity:	61.864	Conservative:	15
Best Local Similarity:	57.998	Mismatches:	35
Query Match:	59.348	Indels:	113
DB:	6	Gaps:	5

US-09-194-164-13 (1-918) x ADA90139 (1-638)

```

QY 7 ATGAAAAAACCGCTATCCCGATCGCATGTTGCACTGGCTGGTTGCGCTACCGTTGGCGAG 66
DB 1 MetLysValThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrValAlaGln 20
QY 67 GCCGATATGTGTGACGAGCTCTCCAGGACCCCTGCTTTGTCTCCAGGGGAAAGAGCC 126
DB 21 AlaAspIleValLeuThrGlnSerProAlaThrLeuSerLeuSerProGlyGlnAla 40
QY 127 ACCCTCTCTGAGGGCGAGTCAGATGAGTGTAGAGCACTAGTACCTGTGTACAGCAG 186
DB 41 ThrLeuSerCysAlaArgAlaSerGlnSerValSerSerSerTyrLeuAlaIlePyrGlnGln 60
QY 187 AAACCTGGCGAGGCTCCCGAGGCTCTCATCTATGTGTGATCCACCGGGCCACTGGCATG 246
DB 61 LysProGlyGlnAlaPheArgLeuLeuIleTyrGlyAlaSerSerArgAlaThrGlyVal 80
QY 247 CCAGACAGGTCAGTCGAGGAGGAGTCCGGGACAGACTTCACCTCCATCAGTACAGTAC 306
DB 81 ProAlaArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
QY 307 GAGCTGAAGATTTTGGACGTATTAATCTGTACAGCACTAGTGTAGTACCTCAGACACT 366
DB 101 GlnProGlnAspPheAlaValTyrTyrCysGlnGlnIleTyrThrProPro----- 118
QY 367 CAGATCATTTCGGCGGAGGAGACCAAGGTGAGATAAACAACTGTGGCTGCACCATCT 426
DB 119 -----ThrPheGlyGlnGlyThrLysValGlnIleLysArgThrValAlaIleProSer 136
QY 427 GTC----- 429
DB 137 ValPheIlePheProProSerAspGlnLeuLysSerGlyThrAlaSerValValCys 156
QY 429 ----- 429
DB 157 LeuLeuAsnAsnPheTyrProArgGlnAlaLysValGlnIlePyrValAlaAspAsnAlaLeu 176
QY 430 ---TTCGCG----- 435
DB 177 GlnSerGlyAsnSerGlnGlnSerValThrGlnAspSerLysAspSerThrTyrSer 196
QY 435 ----- 435
DB 197 LeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlnLysHleValLysValAlaCys 216
QY 436 -----GTTGCGGAGTTCGGGAGGTCGTGATCAGTGAAGTGC----- 474
DB 217 GluValThrPheGlnGlyLeuSerSerProValThrLysSerPheAsnArgGlyGlnAla 236
QY 474 ----- 474
DB 237 MetLysGlnSerThrIleAlaLeuAlaLeuLeuProLeuLeuPheThrProValThrLys 256
QY 475 TCCCAAGTCAGACTGGTGGAGTCTGGGGGAGCGTGTCCAGCTGGAGAGTCCCGTGA 534
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
  
```

```

DB 257 AlaGlnValGlnLeuValGlnSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArg 276
QY 535 CTCTCTGTGACAGCTCTGGATTTCCCTTCAGAAAGTTGCTATGACATGGGTCCGCGAG 594
DB 277 LeuSerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTyrValArgGln 296
QY 595 GCTCTAAGCAAGGGCGTGGAGTGGGTCGAGTATTAATCAATGACAGCACTAAATTC 654
DB 297 AlaProGlyLysGlyLeuGlnIlePyrValSerAlaIleSerGlySerIleSerThrTyr 316
QY 655 TACGAGACTCCGTAAGAGGCGGATTCACCATCTCCAGAGACTTCGAAAGACGAG 714
DB 317 TyrAlaAspSerValLysGlyPheThrIleSerArgAspAsnSerLysAsnThrLeu 336
QY 715 TATCTTAAATGAACAGCTGAGAACTGAGACACGCGTGTCTATTAATCTGTGCGAGAGAT 774
DB 337 TyrLeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrCysAlaArg--- 355
QY 775 CAGACCCCTGTTGGTGACATAGCACACTACTACGTTTGGAGTCTGGGGCAAGGAGCC 834
DB 356 -----TyrGlyGlyAspGlyPheTyrAlaMetAspTyrTyrGlyGlnGlyThr 371
QY 835 ACGTCAACGCTCTCTCAGATCC 858
DB 372 LeuValThrValSerSerAlaSer 379

RESULT 11
ADA91410
ID ADA91410 standard; protein; 638 AA.
XX
XX ADA91410;
XX
XX 20-NOV-2003 (first entry)
XX
XX Anti-Abeta antibody related amino acid sequence #8.
XX
XX antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
XX neurotropic; antiparkinsonian; gene therapy; amyloidogenesis;
XX amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;
XX Alzheimer's disease; motor neuropathy; Down's syndrome;
XX Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
XX Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
XX neuronal disorder; aging.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX MO2003070760-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-EP001759.
XX
XX 20-FEB-2002; 2002EP-00003844.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (MORP-) MORPHOSYS AG.
XX
XX Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretschmar T;
XX Loehning C, Loetscher H, Nordstedt C, Roche C;
XX WPL; 2003-663848/62.
XX
XX New antibody molecule capable of specifically recognizing two regions of
XX the beta-A4 peptide, useful for diagnosing, preventing or treating
XX diseases associated with amyloidogenesis or amyloid-plaque formation
XX (e.g. dementia).
XX
XX Example 1; Fig 2; 312pp; English.
XX
XX The present invention describes an antibody molecule (I) capable of
XX specifically recognising two regions of the beta-A4 peptide/Abeta4. The
XX first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
  
```

CC Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the  
 CC amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Ala-Glu-Asp-Val-  
 CC Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule  
 CC encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host  
 CC cell comprising the vector of (2); (4) preparing (1), comprising  
 CC culturing the host cell of (3) under conditions that allow synthesis of  
 CC (1) and recovering (1) from the culture; (5) a composition comprising (1)  
 CC or an antibody molecule produced by method (4); (6) a kit comprising (1),  
 CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising  
 CC (1); (8) testing the resulting Fab optimisation library by panning  
 CC against Abeta/Abeta4; (9) identifying optimised clones; (10) expressing  
 CC of selected, optimised clones; (11) preparing a pharmaceutical  
 CC composition, comprising optimisation of (1), and formulating the  
 CC optimised antibody/antibody molecule with a carrier, and (12) a  
 CC pharmaceutical composition prepared by method (8). (1) has  
 CC neuroprotective, neurotropic and antiparkinsonian activities, and can be  
 CC used in gene therapy. The antibody molecule (1), nucleic acid molecule,  
 CC vector or host is useful in preparing a pharmaceutical composition for  
 CC the prevention and/or treatment of a disease associated with  
 CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule  
 CC may also be used in preparing a diagnostic composition for the detection  
 CC of the disease mentioned above. The antibody is used for the  
 CC disintegration of beta-amyloid plaques or for passive immunisation  
 CC against beta-amyloid plaque formation. In particular, the disease is  
 CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,  
 CC Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with  
 CC amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,  
 CC amyotrophic lateral sclerosis or neuronal disorders related to aging. The  
 CC present sequence is used in the exemplification of the present invention.

XX Sequence 638 AA;

SO Alignment Scores:

Pred. No.: 3e-73 Length: 638  
 Score: 1016.50 Matches: 225  
 Percent Similarity: 61.86% Conservative: 15  
 Best Local Similarity: 57.99% Mismatches: 35  
 Query Match: 59.34% Indels: 113  
 DB: 6 Gaps: 5

US-09-194-164-13 (1-918) X ADA91410 (1-638)

QY 7 ATGAAAAAAGCGCTATCGGATCGAGTTCAGTGGCTTGGCTACCGTTGGCGAG 66  
 |||  
 Db 1 MetLysThrAlaIleAlaValAlaLeuAlaGlyPheAlaThrValAlaGln 20  
 QY 67 GCCGATATTGTGTGAAGCAGTCTCCAGGCACTCTTGTCTCCAGGGGAAAGGCC 126  
 |||  
 Db 21 AlaAspIleValLeuThrGlnSerProAlaThrLeuSerLeuSerProGlyGlnArgAla 40  
 QY 127 ACCCTCTCTGCGAGGGCGCATGCAAGTGTATGACAGCTACTAGCTGTATCCAGCG 186  
 |||  
 Db 41 ThrLeuSerCysArgAlaSerGlnSerValSerSerSerCysLeuAlaTrpTyrGlnGln 60  
 QY 187 AAACCTGGCCAGGCTCCAGGCTCTCATCTATGATGATCCAGGGGCGCATGGCAG 246  
 |||  
 Db 61 LysProGlyGlnAlaProAlaGlnLeuLeuIleTyrGlyAlaSerSerArgAlaThrGlyVal 80  
 QY 247 CCAGACAGGTTCAAGTGGCAGTGGGTCCGGACAGACTTCACTCCACCATCAGTAGAC 306  
 |||  
 Db 81 ProAlaArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
 QY 307 GAGCCTGAAGATTTTGCAGTGTATCTGTCCAGCAGTATGATGCTCAGACCTCAGAC 366  
 |||  
 Db 101 GlnProGlnAspPheAlaValTyrTyrCysGlnGlnHisIleTyrThrThrProPro----- 118  
 QY 367 CAGATCACTTTCCGCGAGGAGGACCAAGGTGAGAGATCAAGAACTGTGGCTGCACCAT 426  
 |||  
 Db 119 -----ThrPheIleGlnIleGlnThrLysValGlnIleLysArgThrValAlaAlaProSer 136  
 QY 427 GTC----- 429  
 |||  
 Db 137 ValPheIlePheProProSerAspGlnLeuLysSerGlyThrAlaSerValValCys 156

QY 429 ----- 429  
 Db 157 LeuLeuAsnAsnPheTyrProArgGlnAlaLysValGlnTrpLysValAlaAsnAlaLeu 176  
 QY 430 ---TCTGGC----- 435  
 Db 177 GlnSerGlyAsnSerGlnLysSerValThrGlnGlnAspSerLysAspSerThrTyrSer 196  
 QY 435 ----- 435  
 Db 197 LeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlnLysHisLysValTyrLacys 216  
 QY 436 -----GTTGGCGGTTCCGAGGCTGGATCCAGTGGAGAGTGGC----- 474  
 Db 217 GluValThrHisGlnGlyLeuSerSerProValThrLysSerPheAsnArgGlyGlnAla 236  
 QY 474 ----- 474  
 Db 237 MetLysGlnSerThrIleAlaLeuAlaLeuLeuProLeuLeuPheThrProValThrLys 256  
 QY 475 TCCGAGTGCAGCTGTGAGAGTCTGGGAGAGCGGTCTCCAGCCTGGAGGTCCCTGAGA 534  
 :|||  
 Db 257 AlaGlnValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArg 276  
 QY 535 CTCTCTGTGCAAGCTCTTGATTCCTCTTCAAGAGCTTGTATGCACTGGGTCCGCA 594  
 |||  
 Db 277 LeuSerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGln 296  
 QY 595 GCTTAGGCAAGGGGCTGAGAGGTGGTGGCAGTTATATCATATGATGAAGCACTAAATAC 654  
 |||  
 Db 297 AlaProGlyLysGlyLeuGlnIleTrpAlaSerAlaIleSerGlySerGlySerThrTyr 316  
 QY 655 TACGCAAGCTCCGTGAGAGGCGGATTCACCATCTCCAGAGACACTTCCAGAAACGCGT 714  
 :|||  
 Db 317 TyrAlaAspSerValLysGlyArgPheThrIleSerArgAlaAsnSerLysAsnThrLeu 336  
 QY 715 TATCTTAAAAATGACAGCTGAGAACTGAGACACAGCGTGTCTATTACTGTGCCGAGAAT 774  
 |||  
 Db 337 TyrLeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaArg--- 355  
 QY 775 CAGAGCCTGTTGGGAGCTATGACCACTACAGGTGTGACAGTCTGGGCGAAAGGAGCC 834  
 |||  
 Db 356 -----TrpGlyGlyAspGlyPheTyrAlaMetAspTyrTrpGlyGlnIleThr 371  
 QY 835 ACGTCAACGCTCTCTCAGATCC 858  
 |||  
 Db 372 LeuValThrValSerSerAlaSer 379  
 Db  
 RESULT 12  
 ADG74355  
 ID ADG74355 standard; protein; 747 AA.  
 XX  
 AC ADG74355;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 XX MSPEO light chain variable region protein, SEQ ID No 92.  
 XX  
 XX antigen binding; receptor protein tyrosine kinase;  
 KW fibroblast growth factor receptor 3; FGFR3; osteopontin; cytoskeletal;  
 KW neurotrophic; neuroprotective; ophthalmological; antidiabetic; gene therapy;  
 KW bone; cartilage; craniosynostosis; skeletal dysplasia;  
 KW cell proliferative disorder; haematopoietic malignancy;  
 KW hyperproliferative disorder; neurovascular glaucoma;  
 KW macular degeneration; proliferative retinopathy; diabetic retinopathy;  
 KW MSPEO.  
 XX  
 OS Unidentified.  
 OS  
 XX WO2002102972-A2.  
 PN  
 XX 27-DEC-2002.



XX 20-JUN-2002; 2002W0-IL000494.  
 XX  
 XX 20-JUN-2001; 2001US-0299187P.  
 XX  
 XX (PROC-) PROCHON BIOTECH LTD.  
 XX (MORP-) MORPHOSYS AG.  
 XX  
 XX Yayan A, Rom E, Thomassen-Wolf E, Borges E;  
 XX WPI; 2003-175235/17.  
 XX  
 XX New antigen binding portion of an antibody having a specific binding  
 XX affinity for a receptor protein tyrosine kinase, useful for treating bone  
 XX and cartilage related disorders, cell proliferative or hyperproliferative  
 XX disorders.  
 XX  
 XX Claim 42; SEQ ID NO 92; 122pp; English.  
 XX  
 XX The invention relates to a novel molecule comprising the antigen binding  
 XX portion of an isolated antibody having a specific binding affinity for a  
 XX receptor protein tyrosine kinase, and which blocks constitutive  
 XX activation of a receptor protein tyrosine kinase, such as fibroblast  
 XX growth factor receptor 3 (FGFR3). The novel molecules of the invention  
 XX have the following activities: osteopathic, cytostatic, nootropic,  
 XX neuroprotective, ophthalmological, and antidiabetic. The nucleic acids  
 XX encoding the novel molecules of the invention can be used in gene therapy  
 XX to treat disorders. The molecule and nucleic acid molecules are useful  
 XX for treating bone and cartilage related disorders such as  
 XX cranioyostosis (e.g. Muenke coronal craniosynostosis or Crozon  
 XX syndrome with acanthosis nigricans), or skeletal dysplasia (e.g.  
 XX achondroplasia, thanatophoric dysplasia (TD), hypochondroplasia, severe  
 XX achondroplasia with developmental delay and acanthosis nigricans (SADDAN)  
 XX dysplasia), cell proliferative disorders, haematopoietic malignancy (e.g.  
 XX multiple myeloma), hyperproliferative disorders, neurovascular glaucoma,  
 XX macular degeneration or proliferative retinopathy including diabetic  
 XX retinopathy. This sequence represents an MSRO antibody light chain  
 XX variable region peptide relating to the invention.  
 XX  
 XX Sequence 747 AA;  
 XX  
 XX Alignment Scores:  
 XX Pred. No.: 3, 076-73 Length: 747  
 XX Score: 1016, 50 Matches: 225  
 XX Percent Similarity: 61.86% Conservative: 15  
 XX Best Local Similarity: 57.99% Mismatches: 35  
 XX Query Match: 59.34% Indels: 113  
 XX DB: 7 Gaps: 5  
 XX  
 XX US-09-194-164-13 (1-918) x ADG74355 (1-747)  
 QY 7 ATGAAAAAACCGCTATCGCGATGCGAGTGGCTGCTGTTGCGTACCGGTGGCAG 66  
 DB 110 MetLysLysThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrValAlaGln 129  
 QY 67 GCCGATATTGTGTACCGAGTCTCCAGCACCTGTCTTTTCTTCACGAGGAAAGAGCC 126  
 DB 130 AlaAspIleValLeuThrLysSerProAlaThrLysSerLeuSerProGlyGluLysAla 149  
 QY 127 ACCCTCTCTGCGAGGGCCGAGTGTAGTATAGTACAGTATTGACCTGGTACAGAG 186  
 DB 150 ThrLeuSerCysArgAlaSerIleValSerSerSerTyrLeuAlaIleTyrIleGln 169  
 QY 187 AAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGTGATCCAGAGGCGCACTGGCAGT 246  
 DB 170 LysProGlyGlnAlaProArgLeuLeuIleTyrGlyAlaSerSerArgAlaThrGlyVal 189  
 QY 247 CCAGACAGTGTACGTGGCAGTGGGTCCGGGACAGACTTCACTCTACCATCAGTACATG 306  
 DB 190 ProAlaArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 209  
 QY 307 GAGCTGAAGATTTTGGCAGTGTATTACTGTGACAGAGTATGTAGTACCTCAGACACT 366  
 |||||

DB 210 GluProGluAspPheAlaValTyrTyrCysGlnGlnIleSerThrThrProPro----- 227  
 QY 367 CAGATCACTTTGGCGGAGGACCAAGTGGAGATCAAAAGAACTGTGGCTGCACATCT 426  
 DB 228 -----ThrPheGlyGlnGlyThrLysValGluIleLysArgThrValAlaAlaProSer 245  
 QY 427 GTC----- 429  
 DB 246 ValPheIlePheProProSerAspGluGlnLeuLysSerGlyThrAlaSerValValCys 265  
 QY 429 ----- 429  
 DB 266 LeuLeuAsnAsnPheTyrProArgGluAlaLysValGlnTyrLysValAlaAsnAlaLeu 285  
 QY 430 ---CTGGC----- 435  
 DB 286 GlnSerGlyAsnSerGlnGlnSerValThrGlnGlnAspSerLysAspSerThrTyrSer 305  
 QY 435 ----- 435  
 DB 306 LeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlyLysIleValValTyrAlaCys 325  
 QY 436 -----GTTGCGGTTCCGGAGGTGGTGGATCAGTGCAGGTGCG----- 474  
 DB 326 GluValThrIleGlnGlyLeuSerSerProValThrLysSerPheAsnArgGlyGluAla 345  
 QY 474 ----- 474  
 DB 346 MetLysGlnSerThrIleAlaLeuAlaLeuLeuProLeuLeuPheThrProValThrLys 365  
 QY 475 TCCGAGTGCAGCTGTGTGAGTGTGGAGGCGGTCCAGGCGGAGGCGCTGGAGA 534  
 DB 366 AlaGlnValGlnLeuValGlnSerGlyGlyGlyValGlnProGlyGlySerLeuArg 385  
 QY 535 CTCTCCTGTGACGCTCTGATTCCTCCAGAACTTTGCTACTGACATGAGTGGTCCGCGAG 594  
 DB 386 LeuSerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerThrValArgGln 405  
 QY 595 GCTTAGCAAGGGGCTGAGTGGTGGTGCAGTTATATCATATGATGAAAGCACTAAATAC 654  
 DB 406 AlaProGlyLysGlyLeuGluTyrPheValSerAlaIleSerGlySerGlySerThrTyr 425  
 QY 655 TACGAGATCCGCTGTAAGGCGGATTCACATCTCCAGAGACACTCCAGAAACCGGTG 714  
 DB 426 TyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 445  
 QY 715 TATCTAAATAATGAACAGCTGAGAACTGAGACAGCGCTGTATTACTGTGCGAGAT 774  
 DB 446 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArg--- 464  
 QY 775 CAGAGCTGTGGTGAATGACCACTAAGGTTTGGACGTCTGGGCGAAAGGAGCC 834  
 DB 465 -----TyrGlyGlyAspGlyPheTyrAlaMetAspTyrTyrGlyGlnGlyThr 480  
 QY 835 ACGGTCAACGCTCTCTCCAGATCC 858  
 DB 481 LeuValThrValSerSerAlaSer 488  
 RESULT 13  
 AAY44994  
 ID AAY44994 standard; protein; 523 AA.  
 XX AAY44994;  
 XX  
 XX 23-MAY-2000 (first entry)  
 XX  
 XX HD10scFv-CH1-GM-CSF chain.  
 XX  
 XX HD10; single-chain variable fragment; scFv; 17-1A antigen; human; EPCAM;  
 XX epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;  
 XX granulocyte/macrophage colony stimulating factor; heterodimeric;  
 XX CH1-domain; multifunctional compound; heavy chain constant domain;  
 XX immunoglobulin; cytostatic; immunostimulatory; antileukemia; diagnosis;

KM antiproliferative; prevention; treatment; malignant; haematopoietic cell;  
 KM lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.  
 OS Homo sapiens.  
 PN WO200006605-A2.  
 PD 10-FEB-2000.  
 PF 28-JUL-1999; 99WO-EP005416.  
 PR 28-JUL-1998; 98EP-00114082.  
 (MIGR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.  
 PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zetcl F;  
 DR MPI: 2000-195265/17.  
 DR N-PSDB; AA250587.  
 PT New multifunctional compounds useful for preventing and/or treating  
 PT malignant cell growth and for detection and diagnosis.  
 PS Example 10; Fig 55A; 166pp; English.  
 CC The patent discloses heteromolecules which are multifunctional compounds  
 CC producible in a mammalian host cell as a secretable and fully functional  
 CC heterodimer of two polypeptide chains, where one of the polypeptide  
 CC chains comprises a CH1-domain (constant domain of an immunoglobulin  
 CC heavy chain) and the other chain comprises C $\mu$ -domain (constant domain of  
 CC an immunoglobulin light chain). The polypeptide chains further comprise,  
 CC fused to the constant domains at least two (poly)peptides having  
 CC different receptor or ligand functions, where further at least two of the  
 CC different (poly)peptides lack an intrinsic affinity for one another and  
 CC are linked via the constant domains. The heteromolecules have  
 CC cytostatic, immunostimulatory, antileukemia and antiproliferative  
 CC activities. These compounds can be used for diagnosing, preventing and  
 CC treating malignant cell growth related to malignancies of haematopoietic  
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,  
 CC melanomas and sarcomas. The present sequence is the left chain of a  
 CC heteromolecule comprising HD70 single-chain Fv (scFv) fragment N-  
 CC terminally linked to human CH1 domain which bears at its C-terminus the  
 CC human inflammatory cytokine granulocyte/macrophage colony stimulating  
 CC factor (GM-CSF). Plus a hexahistidine sequence for ease of purification.  
 CC HD70 scFv specifically recognises the human epithelial cell adhesion  
 CC molecule (EPCAM) also called 17-1A antigen  
 CC  
 CC  
 SQ Sequence 523 AA;  
 Alignment Scores:  
 Pred. No.: 8,34e-71 Length: 523  
 Score: 986.00 Matches: 193  
 Percent Similarity: 80.65% Conservative: 32  
 Best Local Similarity: 69.18% Mismatches: 38  
 Query Match: 57.56% Indels: 16  
 DB: 3 Gaps: 4  
 US-09-194-164-13 (1-918) x AAY44994 (1-523)  
 QY 28 ATCGAGTTGACCTGGTGTTCGCTACCGTTGCCAGGCGCATATTGTTGAGCGAG 87  
 DB 6 TlelleuDeuDeuValAlaThrAlaThrGlyValHisSerIleuGlnMetThrGln 25  
 QY 88 TCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGACCCCTCTCTCCAGGCGCAGT 147  
 DB 26 SerProSerSerDeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSer 45  
 QY 148 CAGAGTGTAGTACGCTTACGCTGTACGAGGAAAGACTGGCGAGGCTCCAGG 207  
 DB 46 GlnSerIle---SerSerIleuAsnIleTyrGlnGlnIleProGlnIleProPolys 64  
 QY 208 CTCCTCATCATGATGATCCACGAGGCGCATGCGTGCACAGAGTTCACTGGCAGT 267

DB 65 LeuLeuIleTyrTrpAlaSerThrArgGluSerGlyValProAspArgPheSerGlySer 84  
 QY 268 GGGTCCGGACAGACTTACTCTCCATCATAGTAGCTGAGAGCCGAGAGATTTCACAGG 327  
 DB 85 GluSerGlyTrpAsnTyrThrLeuThrIleSerSerIleuGlnProGlnAspPheAlaThr 104  
 QY 328 TATTACTGTCAGACATATGATAGTCACTCCAGACACCTCAGATCACTTTCGGCGAGGG 387  
 DB 105 TyrPheCysGlnGlnSerIleAspSerIleuPro-----IleThrPheIleGlnGly 120  
 QY 388 ACCAAGGTGAGATCAACGAACTGTGCTGACCATCTGTCTTCGGCGGTTCCTCC 447  
 DB 121 ThrArgLeuAspIleGln-----GlyGlyGlyGlySer 131  
 QY 448 GGAAGTGTGTGATTCAGGTGAGGTGGCTCCGAGGTGAGGTGAGGTGAGGTGAGGTG 507  
 DB 132 GlyGlyGlyGlySerGlyGlyGlyGlySerGlyValGlnLeuGlnSerGlyGlyGly 151  
 QY 508 GTGTCGACGCTGGAGGCTCCCTGAGACTCTCTGTGAGGAGCTCTGATTCCTTCAGA 567  
 DB 152 ValValGlnProGlyArgSerIleuArgLeuSerCysAlaAlaSerGlyPheThrPheSer 171  
 QY 568 ACCTTGTATGCACTGGGTCCGCCAGGCTTAGCGAAGGGGCTGAGGTGGTGCAGTT 627  
 DB 172 SerTyrGlyMetHisIleTrpValArgGlnAlaProGlyIleGlyLeuGlnIleTrpValAlaVal 191  
 QY 628 AATTCATATGATGAGAGCACTAATTAATACGAGACTCCGTGAGAGGGCGATTCCACATC 687  
 DB 192 TleSerTyrAspGlySerAsnIleTyrTrpAlaAspSerValIleGlyArgPheThrIle 211  
 QY 688 TCCAGAGACACTCCAGAGACAGCGGTATCTTAAATGAAACAGCCTGAGAACTGAGAGC 747  
 DB 212 SerArgAspAsnSerIleAsnIleThrLeuTyrLeuGlnMetAsnSerIleuArgAlaGluAsp 231  
 QY 748 ACGGTGTCTATCTGTGTCGAGAGATCAGACCTGTGGGTGACTATGAC-----CAC 801  
 DB 232 ThrAlaValTyrTyrCysAlaIleAspMetGlyTyrGlySerGlyTyrArgProTyrTyr 251  
 QY 802 TACTACGCTTGGAGGTCTGCGGCAAGGAGACACGCTGACCGTCCCTCAGAGATCC 858  
 DB 252 TyrTyrGlyMetCaspAlaIleProIleGlnGlyIleThrValThrValSerSerGlyThr 270  
 RESULT 14  
 ID AAY44995  
 AA AAY44995 standard; protein; 524 AA.  
 AC AAY44995;  
 DT 23-MAY-2000 (first entry)  
 DE HD70scFv-Ck-interleukin 2.  
 KW HD70; single-chain Fv fragment; scFv; antibody; 17-1A antigen; human;  
 KW EPCAM; epithelial cell adhesion molecule; inflammatory cytokine; IL-2;  
 KW interleukin-2; Ck-domain; kappa light chain constant domain;  
 KW heteromolecule; multifunctional compound; immunoglobulin; cyostatic;  
 KW immunostimulatory; antileukemia; diagnosis; prevention;  
 KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;  
 KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma.  
 OS Homo sapiens.  
 PN WO200006605-A2.  
 PD 10-FEB-2000.  
 PF 28-JUL-1999; 99WO-EP005416.  
 PR 28-JUL-1998; 98EP-00114082.  
 (MIGR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.  
 PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zetcl F;



CC the invention are useful for treating or inhibiting a skeletal dysplasia,  
 CC craniostenosis or a cell proliferative disorder. The skeletal dysplasia  
 CC is achondroplasia, thanatophoric dysplasia, hypochondroplasia, severe  
 CC achondroplasia with developmental delay or achondroplasia, severe  
 CC dysplasia. The craniostenosis disorder is Muenke coronal  
 CC craniostenosis or Crouzon syndrome with acanthosis nigricans. The cell  
 CC proliferative disorder is tumour progression that is progression of  
 CC transitional cell carcinoma, osteosarcoma, chondrosarcoma, multiple  
 CC myeloma or mammary carcinoma. This sequence represents the protein  
 CC derived from a Fab expression vector relating to the protein tyrosine  
 CC kinase inhibitor of the invention  
 CC  
 XX

Sequence 628 AA:

Alignment Scores:  
 Pred. No.: 1,05e-69 Length: 628  
 Score: 972.50 Matches: 215  
 Percent Similarity: 60.854 Conservative: 15  
 Best Local Similarity: 56.888 Mismatches: 35  
 Query Match: 56.778 Indels: 113  
 DB: 6 Gaps: 5

US-09-194-164-13 (1-918) x AB038670 (1-628)

QY 37 GCACTGGCTGGTTGGCTACCGTTGGCGAGCCGATATTGTGTGACGAGTCTCCAGGC 96  
 Db 1 AAlaLeuAlaGlyPheAlaThrValAlaGlnAlaAspIleValLeuThrInserProAla 20  
 QY 97 ACCCTGCTTTTGTCTCCAGGGAAGAGCCACCTCTCTCGAGGCGCAGTCAAGTGT 156  
 Db 21 ThrLeuSerLeuSerProGlyGlnArgAlaThrLeuSerCysArgAlaSerGlnSerVal 40  
 QY 157 AGTAGAGCTTACTTACCTGTGTACGACGAAACCTGSCCAGGCTCCAGGCTCTCATC 216  
 Db 41 SerSerSerTyrLeuAlaThrTyrGlnGlnLysProGlyGlnAlaProArgLeuLeuIle 60  
 QY 217 TATGTGTGATCCACCGAGGCGCATGCGACAGAGTTTCAGTGGCAGTGGTCCGGG 276  
 Db 61 TyrGlyAlaSerSerArgAlaThrGlyValProAlaArgPheSerGlySerGly 80  
 QY 277 ACAGACTTCACTCTCACCATCATGAGTGTGAGCTGAGACCTGAAGATTTTGCATGTTACTGT 336  
 Db 81 ThrAspPheThrLeuThrIleSerSerLeuGlnProGlnAspPheAlaValTyrTyrCys 100  
 QY 337 CAGCAGTATGTAGCTCAGCTCAGACACCTCAGATCATTTCGCGAGGAGCAAGAGTG 396  
 Db 101 GlnGlnIleTyrThrThrProPro-----ThrPheGlyGlnGlyThrIlyVal 116  
 QY 397 GAGATCAACGAACTGTGGCTGACCATCTGTC----- 429  
 Db 117 GluIleLysArgThrValAlaAlaProSerValPheIlePheProProSerAspGlnGln 136  
 QY 429 ----- 429  
 Db 137 LeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGlnAla 156  
 QY 430 -----TCTGGC----- 435  
 Db 157 LysValGlnTyrLysValAlaAspAsnAlaLeuGlnSerGlyAsnSerGlnGlnSerValThr 176  
 QY 435 ----- 435  
 Db 177 GluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAla 196  
 QY 436 -----GGTGGCGGTTCCGA 450  
 Db 197 AspTyrGlnLysHisLysValTyrAlaCysGlnValThrHisGlnIlyLeuSerSerPro 216  
 QY 451 GGTGTGATCAAGTGGAGGTGC----- 474  
 Db 217 ValThrLysSerPheAsnArgGlyGlnAlaMetLysGlnSerThrIleAlaLeuAlaLeu 236  
 QY 475 -----TCCAGGTGACGCTGGTGAAGTCTGGGGGA 504

Db 227 LeuProLeuLeuPheThrProValThrIlySalGlnValGlnLeuValGlnSerIlyGly 256  
 QY 505 GCGGTGTCCAGCCCTGGAGAGTCCCTGAGACTTCTGTGACGCTCTGAGATTCCCTTC 564  
 Db 257 GlyLeuValGlnProGlyGlySerLeuArgLeuSerCysAlaAlaSerGlyPheThrPhe 276  
 QY 555 AGAGCTTGTCTATGCACTGGGTCCGACAGCTCTAGGCAAGGGCTGAGTGGGTGGCA 624  
 Db 277 SerSerTyrAlaMetSerTyrValArgGlnAlaProGlyLysGlyLeuGlnTyrPValSer 296  
 QY 625 GTTATATATGATGAGACACTAAATATACGAGACTCCGTGAAAGGCGGATTCACC 684  
 Db 297 AlaIleSerGlySerGlyGlySerThrTyrTyrAlaAspSerValLysGlyArgPheThr 316  
 QY 685 ATCTCCAGAGACACTTCCAGAAACAGGTGTATCTTAAAAATGACAGCCTGAGAACTGAG 744  
 Db 317 IleSerArgAspAsnSerLysAsnThrLeuTyrLeuGlnMetAsnSerLeuArgAlaGln 336  
 QY 745 GACAGGCTGTCTATTACTGTGCGAGAGATCAGAGCCTGTGGTGACTATGACACACTAC 804  
 Db 337 AspThrAlaValTyrTyrCysAlaArg-----TyrGlyGlyAspIlyPhe 351  
 QY 805 TACGGTTTGAAGTCTGGGCGCAAGGAGCAACAGGTACCGTCTCTCTCAGATCC 858  
 Db 352 TyrAlaMetAspTyrTyrPheGlyGlnIlyThrLeuValThrValSerSerAlaSer 369

Search completed: February 18, 2005, 08:42:17  
 Job time : 106.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 18, 2005, 08:27:58 ; Search time 22.5 Seconds

(without alignments)  
6091.364 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 1713  
Sequence: 1 GAATTCATGAAAAAACCAGC.....ATCACCATTAGTGAAGCTT 918

## Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

MODEL=frame+ n2p.model -DEV=x1h  
-Q=/cgn2\_1/USPRO/epool/US09194164/runat.16022005.122614.6047/app.query.fasta\_1.1095  
-DB=Issued Patents AA -QFMT=fastan -SUFFIX=ra1 -MINMATCH=0.1 -LOOBL=0  
-LOOBL=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdt  
-LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09194164@cgn 1.1.22 @runat.16022005.122614.6047 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOC  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRAD=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1573	91.8	304	US-08-862-124-14	Sequence 14, Appl
2	1451.5	84.7	287	US-08-862-124-17	Sequence 17, Appl
3	928	54.2	4	US-09-203-958A-2	Sequence 2, Appl
4	926.5	54.1	456	US-09-495-880A-11	Sequence 11, Appl
5	892	52.1	283	US-09-420-592A-6	Sequence 6, Appl
6	892	52.1	283	US-09-985-442-6	Sequence 6, Appl
7	892	52.1	283	US-09-983-580-6	Sequence 6, Appl
8	887	51.8	263	US-09-069-821-3	Sequence 3, Appl
9	887	51.8	263	US-09-956-086-3	Sequence 3, Appl
10	887	51.8	263	US-09-956-087-3	Sequence 3, Appl
11	865	50.5	354	US-09-393-627B-28	Sequence 28, Appl
12	827.5	48.3	240	US-08-488-113B-147	Sequence 147, Appl

13	827.5	48.3	240	US-08-477-484B-147	Sequence 147, App
14	827.5	48.3	240	US-08-646-360-147	Sequence 147, App
15	827.5	48.3	240	US-08-839-765-147	Sequence 147, App
16	827.5	48.3	240	US-09-136-389-147	Sequence 147, App
17	827.5	48.3	240	US-09-610-838-147	Sequence 147, App
18	827.5	48.3	240	US-09-711-485-147	Sequence 147, App
19	808.5	47.2	409	US-09-554-765-14	Sequence 14, Appl
20	805	47.0	408	US-09-554-765-15	Sequence 15, Appl
21	784	45.8	271	US-08-400-115-4	Sequence 4, Appl
22	784	45.8	374	US-09-646-028-15	Sequence 15, Appl
23	779.5	45.5	491	US-10-011-125A-2	Sequence 2, Appl
24	777	45.4	599	US-08-442-542-18	Sequence 18, Appl
25	777	45.4	599	US-08-765-469-18	Sequence 18, Appl
26	766	44.7	298	US-09-318-661-2	Sequence 2, Appl
27	766	44.7	298	US-09-883-758-2	Sequence 2, Appl
28	756	44.1	244	US-08-392-338A-13	Sequence 13, Appl
29	756	44.1	244	US-09-166-750-13	Sequence 13, Appl
30	756	44.1	244	US-09-166-093-13	Sequence 13, Appl
31	756	44.1	244	US-09-172-019-13	Sequence 13, Appl
32	756	44.1	244	US-09-166-094-13	Sequence 13, Appl
33	756	44.1	244	US-09-443-213-13	Sequence 13, Appl
34	755	44.1	239	US-08-860-174A-2	Sequence 2, Appl
35	744	43.4	242	US-08-224-591-14	Sequence 14, Appl
36	744	43.4	242	US-08-928-338A-23	Sequence 23, Appl
37	744	43.4	242	US-08-928-789-14	Sequence 14, Appl
38	744	43.4	242	US-09-166-750-23	Sequence 23, Appl
39	744	43.4	242	US-09-166-093-23	Sequence 23, Appl
40	744	43.4	242	US-09-172-019-23	Sequence 23, Appl
41	744	43.4	242	US-09-166-094-23	Sequence 23, Appl
42	744	43.4	242	US-09-443-213-23	Sequence 23, Appl
43	744	43.4	244	PCT-US93-11138-14	Sequence 14, Appl
44	744	43.4	285	US-09-318-661-4	Sequence 4, Appl
45	744	43.4	285	US-09-883-758-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-08-862-124-14  
; Sequence 14, Application US/08862124  
; Patent No. 6207153  
GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; APPLICANT: Mailfi, Pradip K.  
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Morrieon & Foerster LLP  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/862,124  
; FILING DATE: 22-MAY-1997  
; CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
; NAME: Lehnardt, Susan K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792

TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 304 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-862-124-14

## Alignment Scores:

Pred. No.:	3e-124	Length:	304
Score:	1573.00	Matches:	302
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	91.83%	Indels:	0
DB:	3	Gaps:	0

US-09-194-164-13 (1-918) x US-08-862-124-14 (1-304)

```

QY 1 GAATTGATGAAAAAACCCTATCGGATCGAGTTGCGACTGGCTGCTTCCGTACCGTT 60
    |||
DB 1 GluphemeclyssthzraiaaleaialaValaaleuAaaglypheaIatThrVal 20

QY 61 GGGGAGCCGATATTGTGTGAAGCAGTCTCCAGGACCGCTTGTCTCCAGGGGAAA 120
    |||
DB 21 AlaGlnAlaaspIleValleuThrGlnserProGlyThrleuserleuserProGlyGln 40

QY 121 AGAGCCACCTCTCTGCGAGGGCGAGTCAAGTGTATAGCAGCTACTTACCTGGTAC 180
    |||
DB 41 ArgAlaThrleuserCysaArgAlaaserGlnserValserSerSerlyrleuAatpTyr 60

QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTTAATGGTGATCCACGAGGCACT 240
    |||
DB 61 GlnGlnLysProGlyGlnAlaProaArgleuLeuIleTyrGlyAlaSerThrArgAlaThr 80

QY 241 GGCATGCGCAGACAGTTGAGTGGGAGTCCGGGAGCAGACTTCACTCTCCACCATCAGT 300
    |||
DB 81 GlyMeProaSpaRphseSerGlyserGlyserGlyThrAaSpheThrleuThrIleSer 100

QY 301 AGACTGAGACCTGAAGATTGTCAGTGTATTAAGTCAAGATGATGATGATGATGATGAT 360
    |||
DB 101 ArgleuGlnProGlnuSpheAlaValTyrTyrCyGlnGlnIleTyrGlySerSerProGln 120

QY 361 AACCTTCAGATCACTTTCGGCGAGGAGCAGAGTGAAGATCAAAGAACTGTGGTGA 420
    |||
DB 121 ThrProGlnIleThrheGlyGlyGlyThrLysValGlnIleLysArgThrValaAla 140

QY 421 CCATCTGTCTGGCGGCGGCGGTTCCGAGGAGTGAATCAAGTGAAGTGGCTCCGAG 480
    |||
DB 141 ProserValSerGlyGlyGlySerGlyGlyGlySerGlyGlySerGlyGlySerGln 160

QY 481 GTGCACTGGTGAAGTCTGGGGAGGCGTGTTCAGCCTGGAGAGTCCCTGAGACTCTCC 540
    |||
DB 161 ValGlnLeuValGlnSerGlyGlyGlyValGlnProGlyArgSerleuArgleuSer 180

QY 541 TGTGCAAGCTCTGGATTTCCCTTCAAGAGCTTGTGATGACTGGGTCGCCAGGCTCTA 600
    |||
DB 181 CysAlaAlaSerGlyPheProPheArgSerPheAlaMeChIeTyrValArgGlnAlaLeu 200

QY 601 GGCAGAGGGCTGAGGAGGAGGAGTATATCATATGATGAAGCACTAAATCTACGCA 660
    |||
DB 201 GlyLysGlyLeuGlnIleTyrValAlaValIleSerTyrAspGlySerThrIleTyrTyrAla 220

QY 661 GACTCCGTGAAGGCGCATTCACATCTCCAGAGCACTTCCAGAAACGCGTATCTTA 720
    |||
DB 221 AapSerValLyselIyArpHeThrIleSerArgaSpThrSerIyAaenThrValTyrLeu 240

QY 721 AAAATGAACGCTTGAGAACTGAGGACAGGCTGTCTATTAATCTGTGCGAGATTCAGAG 780
    |||
DB 241 LysMeAsnSerleuArgThrGlnaAspThrAlaValTyrTyrCyAlaArgaSpGlnSer 260

QY 781 CGTTGGGATGATATGATACCACTACGCTTGGAGTGGGCGAAAGGACCAAGGCGC 840
    |||

```

```

DB 261 LeuLeuGlyAspTyrAspHisIeTyrGlyLeuAspValTrrpGlyLysGlyThrThrVal 280
QY 841 ACCGTCCTCGAGATCCGAACAAAACCTGATCAGCGAAGAGATGTGAACCATACCAT 900
    |||
DB 281 ThrValSerSerGlySerGlnGlnLysleuIleSerGlnGlnAspLeuAaHisIleHis 300

QY 901 CACCAT 906
    |||
DB 301 HisHis 302

```

## RESULT 2

US-08-862-124-17

Sequence 17, Application US/08862124

Patent No. 6207153

GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

APPLICANT: Maili, Pradi K.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT

SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE

FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND

DETECTION OF CANCERS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSER: Morrison &amp; Foerster LLP

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/862,124

FILING DATE: 22-MAY-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Lehnardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 287 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-862-124-17

## Alignment Scores:

Pred. No.:	4.91e-114	Length:	287
Score:	1451.50	Matches:	283
Percent Similarity:	93.71%	Conservative:	0
Best Local Similarity:	93.71%	Mismatches:	2
Query Match:	84.73%	Indels:	17
DB:	3	Gaps:	1

US-09-194-164-13 (1-918) x US-08-862-124-17 (1-287)

```

QY 1 GAATTGATGAAAAAACCCTATCGGATCGAGTTGCACTGGCTGCTTCCGTACCGTT 60
    |||
DB 1 GluphemeclyssthzraiaaleaialaValaaleuAaaglypheaIatThrVal 20

QY 61 GGCAGGCGCATATTGTGTGAAGCAGTCTCCAGGACCGCTTGTCTTGTCTTCAGGGAAA 120
    |||
DB 21 AlaGlnAlaaspIleValleuThrGlnserProGlyThrleuserleuserProGlyGln 40

```

```

QY 121 AGAGCCACCTCTCTGAGGCGGAGGCTGAGGTTAGTACGAGCTTACTGCTGTAC 180
DB 41 AGAATHLHLSERCYEARHGAASERVSERVSERVSERYLEULATRYR 60
QY 181 CAGCAGAAACCTGGCAGGCTCCAGGCTCTCATCTATGTCATCCAGGCGCACT 240
DB 61 GINGLNLVPRGGLYGLMLAIPROARGLLEULIETRYGLVLSERTHRGALATHR 80
QY 241 GGCATGCCAGACAGGTTGAGTGCGAGTGGGTCGGGAGACAGACTTCACTCCATCACT 300
DB 81 GYMETPROASPARPHERSERGLYSERGLYTHRASPHERTHREUTHRILESER 100
QY 301 AGACGTGGAGCCGAGATTTTGCAGGTATTACTGTCGACGATGATGATGATGATGATGAT 360
DB 101 ARGLEUGLUPROGLIUSPHEALAVALLYTRYCYVGLNGLNTRYGLYSERSEPROGLN 120
QY 361 ACACCTCAGATCACTTTCCGCGAGGAGGACCAAGTGGAGATCAAAAGAACTGGCTGCA 420
DB 121 THRPROGLNIETHRPHEGLYGLYTHRYVALGLNLIELYHARGHTRVALAALA 140
QY 421 CCATCTGTCTCGCGGTGGCGGTCCTCCGAGGTGTGATCAGTGGAGGTGGCTCCAG 480
DB 141 -----SERGLYGLN 143
QY 481 GTGCACTGTGGAGTCTGGGGGAGGCGGTGTCAGCTTGGAGGTCCCTGAGACTTCC 540
DB 144 VALGLNLVLAVALSERGLYGLYVALVALGLNPROGLYARGSERLEULARGLEUSER 163
QY 541 TGTGCAAGCTGTGATTCCTTCCAGAACTTGTGATGATGATGATGATGATGATGATGAT 600
DB 164 CYSAALAAASERGLYPHEPROPHARGSERPHEALAMEHLETRVALARGGLMLALEU 183
QY 601 GGCAGAGGCTGTGAGTGGTGGCAGTTATATCATATGATGAGAACTAAATATCTACGCA 660
DB 184 GLYLSGLYLEUGLUTRPVALAVALIIESERTYRASPGLYSERTHYRTRYRILA 203
QY 661 GACTCCGTGAGAGGCGCATTCACCATCTCCAGAGACACTTCCAAAGAACGGGTATCTA 720
DB 204 AAPSERTVALYSGLYARSPHERTHRILESERAPSPRTHSERLYASANTHRVALYTRYEU 223
QY 721 AAAATGAACAGCCTGAGAACTGAGAGACAGCGCTGTCTATTACTGCGGAGAGATCAGAC 780
DB 224 LYSMETANSERLERLHARGHTRHVALAVALIYTRYCYVALIARGHAPGLINER 243
QY 781 CTGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 244 LEULEUGLYASPTYARSPHERTRYRGLYLEUASBPVALITRPGLYLGLYTHRTRVAL 263
QY 841 ACCGCTCTCTCAGATCCGAGACAAAAGTATGATCAGCGAAAGATCTGAACCATCACT 900
DB 264 THRVALSERSERGLYSERGLNGLYLEULIESERGLYUASPLAUSNHIHSHLS 283
QY 901 CACCAT 906
DB 284 HISHLS 285

```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRY
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-203-958A-2

Alignment Scores:
Pred. No.: 5,65e-70 Length: 352
Score: 928.00 Matches: 192
Percent Similarity: 75.43% Conservative: 26
Best Local Similarity: 66.44% Mismatches: 45
Query Match: 54.17% Indels: 26
DB: 4 Gaps: 5

US-09-194-164-13 (1-918) x US-09-203-958A-2 (1-352)
QY 52 GCTACCGTTGGCGAGGCGGATATGTTGACGAGTCTCCAGGACCCCTGTCTGTCT 111
DB 32 AAGINPROALAARGSERASPILLEGLNLEUTHRGINSERPROSERSERLEUSERAASER 51
QY 112 CCAGGGGAGAGACCCCTCTCCGAGGCGGAGCTCAGAGTGT----- 156
DB 52 VALGLYASBPARGVALTHRIETHCYLSYSSERBSERGLNSERVALLEUTRYSERSERAN 71
QY 157 AGTAGCAGCTACTTATGCTGTGATACGAGAGAACTGGCCAGGCTCCAGGCTCTCATC 216
DB 72 GLNLSAANTYRLEUALITRPTRYGLNGLNINLYSPROGLYLSALAPROLYLEULEULIE 91
QY 217 TATGTTGATCCACGAGGCGCACTGGCATGCCAGACAGTTCAGTGGAGTGGCTCCGGG 276
DB 92 TYRTPALASERTHARGLSERGLYALPROSERARGPHERSERGLYSERGLY 111
QY 277 ACAGACTTCACTTCACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 336
DB 112 THRASPHERTHRPHETHRILESERSERLEUNGLNPROGLIUALIETHRYTRYRYS 131
QY 337 CAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 396
DB 132 HISEGLNYRLEUSER-----TRPTHRPHGLYGLNGLYTHRYLSVAL 146
QY 397 GAGATCAACGAGACTGTGGCTGACCATCTGTCTCTGCGGTGGCGGTTCGAGAGTGT 456
DB 147 GLULIYSSER-----SERGLYGLYGLYSERGLYGLYGLY 159
QY 457 GGATCAGGTGAGAGTGGCTCCAGAGTGCAGCTGTGAGTCTGGGGAGGCGGTGTCCAG 516
DB 160 GLYSERGLYGLYGLYSERGLYVALGLNLEUVALGLNLSERGLYGLYVALVALGLN 179
QY 517 CCTGGAGAGTCCCTGAGACTCTCCGTGAGCAGCTGTGATTCCTTCCAGAAAGCTTGTCT 576
DB 180 PROGLYARGSERLEULARGLEUSERCYSSERSESERGLYPHELEPHESERASPSANTYR 199
QY 577 ATGCACTGGGTCCGCGAGGCTCTAGGCAAGGCGGTGAGTGGGTGAGTATATCATAT 636
DB 200 METRYTRTPVALARGGLNALAPROGLYLSGLYLEUGLUTRPVALALATHRILESERAP 219
QY 637 GATGAGACCTAAATATCAAGCAGACTCCGTGAAGGCGGATTCACCATCTCCAGAGAC 696
DB 220 GLYGLYSERYRTHRYTRYRPROASPSERVALIYSGLYARGPHERTHRILESERARGAP 239
QY 697 ACTTCCAGAGACAGGCTATCTAAATAATGAACGCTGAGAACTGAGAGACAGCGCTGC 756
DB 240 ASNSERYASANTHRLEUPLHARGHTRHVALIYSGLYARGPHERTHRILESERARGAP 259
QY 757 TATTACTGTGCGAGAGATCAGAGAGCTGTGGGTGATATGACCACTACTAGAGTTGGAC 816
DB 260 TYRPHCYSAALAYG-----GLYTRYTRYRARGTRYRGLNGLYALAMEKASBP 274
QY 817 GTCTGGGCAAGAGGACCAAGGCTCAGCGTCTCTCAGAA-----TCCGAAACA 864

```

```

Db      275 TyrTpglyGlnGlyThrProValThrValSerSerProArgLeuGlnValAspGln 294
QY      865 AAACGATCAGCGAAGAAAGATCTGAAC 891
        |||
Db      295 LysLeuIleSerGluGluAspLeuAsn 303
        |||

RESULT 4
US-09-495-880A-11
; Sequence 11, Application US/09495880A
; Patent No. 6667150
; GENERAL INFORMATION:
; APPLICANT: RUDERT, FRITZ
; APPLICANT: GE, LIMING
; APPLICANT: ILAC, VIC
; TITLE OF INVENTION: NOVEL METHOD AND PHASE FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: NOCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIC
; FILE REFERENCE: MORPHO/9
; CURRENT APPLICATION NUMBER: US/09/495,880A
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: PCT/EP98/04836
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: EP 97 11 3319.4
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 456
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ompA-flag-scfv (anti-
; OTHER INFORMATION: HA6)-gene IIIs encoded by phage vector fhagla (circular)
US-09-495-880A-11

Alignment Scores:
Pred. No.:      8, 08e-70      Length:      456
Score:          926.50        Matches:      130
Percent Similarity: 75.42%    Conservative: 37
Best Local Similarity: 63.12% Mismatches:    49
Query Match:    54.09%       Indels:       25
DB:             4            Gaps:          6

US-09-194-164-13 (1-918) x US-09-495-880A-11 (1-456)
QY      7 ATGAAAAAACCCTATCGGATCGAGTTCAGTGGCTGTTCCCTACCGTTGCCGAG 66
        |||
Db      1 MetLysLysThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrValAlaGln 20
        |||
QY      67 GCC-----GATTGTGTGACGCGAGTCCGAGGACCCCTGCTTGTGCTCCAGG 117
        |||
Db      21 AlaAspTyrLysAspIleValMetIleGlnSerProSerSerLeuThrValThrAlaGly 40
        |||
QY      118 GAAAGAGCCACCTCTCTCCAGGAGGAGTCAAGATGTTAGTACAGC----- 165
        |||
Db      41 GluLysValThrMetSerGlyThrSerSerGlnSerLeuPheAsnSerGlyLysGlnLys 60
        |||
QY      166 ---TACTTACCTGTGATACAGCAAGAACTGCGCAGGCTCCAGGCTCTCATCTTGTGT 222
        |||
Db      61 AsnTyrLeuThrTyrTyrGlnGlnLysProGlyGlnProGlySerValLeuIleTyrTrp 80
        |||
QY      223 GCATTCACGAGCGCCACCTGCGAGTTCAGGAGTTCAGGAGGAGTTCGCGGAGCAGAC 282
        |||
Db      81 AlaSerThrArgLysIleSerGlyValProAspArgPheThrIleSerIleSerGlyLysTrpAsp 100
        |||
QY      283 TTCACCTCAGCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 342
        |||
Db      101 PheThrLeuThrIleSerSerValGlnAlaGluAspLeuAlaValTyrTyrCysGlnAsn 120
        |||
QY      343 TATGTAGTCACTCAGTACAGACCTCAGATCATCTTTCGCGGAGGAGCAAGGTGAGATC 402
        |||
Db      121 AspTyrSerAsnPro-----LeuThrPheGlyGlyGlyThrIleGluGluLeu 136

```

```

QY      403 AAAGCACTGAGGCTGACCACTCT-----GTCTTGGCCGT 438
        |||
Db      137 LysArgAlaGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGly 156
        |||
QY      439 GCGCGTTCCGAGAGTGTGATCAGGTGAGAGTGGCTCCAGGTGACAGTGTGAGTCT 498
        |||
Db      157 GlyIleSerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly 176
        |||
QY      499 GGGGAGCGCTGTCACAGCTGCGAGAGTCCCTGAGTCTCTGTCGAGCCCTGAGATTC 558
        |||
Db      177 GlyIleAspLeuValLysProGlyLysSerLeuLysSerCysAlaIleSerGlyPhe 196
        |||
QY      559 CCTTCAGAGCTTGTGATGATCAGTGGTCCGAGCTTACAGGAGGAGGCTGAGTGG 618
        |||
Db      197 SerPheSerSerTyrGlyMetSerTyrValArgIleThrProAspLysArgLeuIleTrp 216
        |||
QY      619 GTGGCAGTTATATCATATGATGAGAAACACTAAATCTACGACAGTCCGTGAAGGCCGA 678
        |||
Db      217 ValAlaThrIleSerAsnGlyGlyGlyTyrThrTyrTyrProAspSerValLysGlyArg 236
        |||
QY      679 TTCACCATCTCCAGAGACACTTCCAGAAACCGGTGATCTTAAATGACAGCTGAGA 738
        |||
Db      237 PheThrIleSerArgAspAsnAlaLysAsnThrLeuTyrLeuGlnMetSerLeuLys 256
        |||
QY      739 ACTGAGACACAGGCTGTATTAATTAATGTCGAGAGATCAGAGCTGTGGTGAATGAC 798
        |||
Db      257 SerGluAspSerAlaMetTyrTyrCysAlaThrArgGluArg-----TyrAsp 272
        |||
QY      799 CACTACACGCTTGTGAGAGCTCTGGGGCAAGGAGCACCGGTGACCTCTCTCAGAGATCC 858
        |||
Db      273 Glu---AsnGlyPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAlaSerGly 291
        |||
QY      859 GAA 861
        |||
Db      292 Glu 292

```

```

RESULT 5
US-09-420-592A-6
; Sequence 6, Application US/09420592A
; Patent No. 6333396
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6333396el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300001
; CURRENT APPLICATION NUMBER: US/09/420,592A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 283
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Kabat
; OTHER INFORMATION: Consensus
; NAME/KEY: UNSURE
; LOCATION: (232)
; OTHER INFORMATION: May be any amino acid.
; NAME/KEY: UNSURE
; LOCATION: (234)
; OTHER INFORMATION: May be any amino acid.
; NAME/KEY: UNSURE
; LOCATION: (239)
; OTHER INFORMATION: May be any amino acid.
US-09-420-592A-6

Alignment Scores:
Pred. No.:      5, 71e-67      Length:      283
Score:          892.00        Matches:      181

```



Percent Similarity:	76.92%	Conservative:	29
Best Local Similarity:	66.30%	Mismatches:	3
Query Match:	52.07%	Indels:	16
DB:	3	Gaps:	5

US-09-194-164-13 (1-918) X US-09-420-592A-6 (1-283)

QY 70 TATATTGGTGGACCCAGCTCTCCAGGACCCGCTCTTGGTCTCCAGGGGAAAGACACCC 129  
 Db 1 AapIleGIaMetThrGInSerProSerSerLeuSerAlaSerValGlyAapArgValThr 20  
 QY 130 CTCCTCTGACGGGCCAGTCCAGAGT-----AGTACGAGCTACTTACGCTGTACCG 183  
 Db 21 IetThrCyAArgAlaSerGInSerLeuSerValSerIleSerAenTyIleuAlaTyrGIn 40  
 QY 184 CAGAAACCTGGGCGAGCTCCGAGGCTCCATCTATGTGATCCACACGAGGCCACTGGC 243  
 Db 41 GInLysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGInSerGly 60  
 QY 244 ATGCCAGACAGGTTCACTGCGAGCTGGTCCGGAGACAGACTTCACCTCCAGTACAGT 303  
 Db 61 ValProSerArgPheSerGlySerGlyGerglyThrAapPheThrLeuThrIleSerSer 80  
 QY 304 CTGAGAGCCTGAAGAATTTTGGCAGTGTATTACTGTCAAGCAGTATGTAGTCACTCAG 363  
 Db 81 LeuGInProGlyAapPheAlaThrTyrTyrCyGInGInTyrAAsSer-----Leu 97  
 QY 364 CCTCAGATCATCTTTCGCGAGGAGGACCAAGGAGAGATCAAAACGAACCTGTGGCTGAC 423  
 Db 98 ProGluTyrPThrPheGlyGInGlyThrIysValGluIleLysGlySer----- 113  
 QY 424 TCTGTCTCTGCGCGGTGGCGTTCGCGAGGTGGTGTGATCAGGTGAGGTGGCTCCAGGT 483  
 Db 114 -----ThrSerGlySerGlyLysProGlySerGlyGInGlySerThrIleGlyVal 131  
 QY 484 CAGCTGGTGGAGTCTGGGGGAGCGGTGTCAGCCTCGGAGAGTCCCTGAGACTCCCTGT 543  
 Db 132 GInLeuValGInSerGlyGlyLysLeuValGInProGlyGlySerLeuArgLeuSerCys 151  
 QY 544 GCAGCCTCTGGATTCCTCCCTTCAGAACTTTGTCTATGACTGGGTCCGACGCTTACGC 603  
 Db 152 AlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTyrValArgGlnAlaProGly 171  
 QY 604 AAGGGGCTGGAGTGGTGGCAGTATATCA-----TATGATGAGACACTAAATATCAC 657  
 Db 172 LysGlyLeuGInTyrPValSerValIleSerGlyLysThrAapGlyGlySerThrTyrTyr 191  
 QY 658 GCAGACTCCGGAAGGGGCGGATTCACCATCTCCAGACACACTTCAAGAAACCGGTGAT 717  
 Db 192 AlaAapSerValLysGlyArgPheThrIleSerAlaAapAenSerLysAenThrLeuTyr 211  
 QY 718 CTAAATAATGAACAGCCTTGAGAACTGAGAGACACGGTGTCTATTACTGTGCGAGATCAG 777  
 Db 212 LeuGInMetAenSerLeuArgAlaGluAapPheThrAlaValTyrTyrCyAlaAlaGlyArg 231  
 QY 778 -----AGCCTGTGGGTGAGCTATACCAACACTACTACGGTTTGAGACTCTGGGGCAA 828  
 Db 232 \*\*\*Gly\*\*\*SerLeuSerGly\*\*\*TyrTyrTyrTyrThrTyrPheAapTyrTrpGlyGIn 251  
 QY 829 GGGACCAACGGTACACCGTCTCTCCAGATCCAGCAAAAA 867  
 Db 252 GlyThrLeuValThrValSerSerTyrLysLysLysLys 264  
 RESULT 6  
 US-09-985-442-6  
 ; Sequence 6, Application US/09985442  
 ; Patent No. 6692942  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Filpula, David R.  
 ; APPLICANT: Wang, Maoliang  
 ; APPLICANT: Whitlow, Marc D.  
 ; TITLE OF INVENTION: No. 6692942e1 Method for Targeted Delivery of Nucleic Acids  
 ; FILE REFERENCE: 0977\_2300003

	/	CURRENT APPLICATION NUMBER:	US-09/985,442
	/	PRIOR FILING DATE:	2001-11-02
	/	PRIOR APPLICATION NUMBER:	09/420,592
	/	PRIOR FILING DATE:	1999-10-19
	/	PRIOR APPLICATION NUMBER:	60/104,949
	/	PRIOR FILING DATE:	1998-10-20
	/	NUMBER OF SEQ ID NOS:	13
	/	SOFTWARE:	Patentin Ver. 2.1.1
	/	SEQ ID NO:	6
	/	LENGTH:	283
	/	TYPE:	PRN
	/	ORGANISM:	Artificial Sequence
	/	FEATURE:	
	/	OTHER INFORMATION:	Description of Artificial Sequence: Kabat
	/	OTHER INFORMATION:	Consensus
	/	NAME/KEY:	UNSURE
	/	LOCATION:	(232)
	/	OTHER INFORMATION:	May be any amino acid.
	/	NAME/KEY:	UNSURE
	/	LOCATION:	(234)
	/	OTHER INFORMATION:	May be any amino acid.
	/	NAME/KEY:	UNSURE
	/	LOCATION:	(239)
	/	OTHER INFORMATION:	May be any amino acid.
	/	US-09-985-442-6	
	/	Alignment Scores:	
	/	Pred. No.:	5,71e-67 Length: 283
	/	Score:	892.00 Matches: 181
	/	Percent Similarity:	76.92% Conservative: 29
	/	Best Local Similarity:	66.30% Mismatches: 47
	/	Query Match:	52.07% Indels: 16
	/	DB:	Gaps: 5
	/	US-09-194-164-13 (1-918) x US-09-985-442-6 (1-283)	
OY		70 GATATTGTTGAGCGCAGTCTCCAGGCACCCGTCTTGTCTCCAGGGGAAGAACCACC	1299
Dd		1 AaplliegImethrThgInserProberSerLeuSerValGllyAsparValThr	20
OY		130 CTCCTCGTCAGGGCCAGTCAGTGST-----AGTAGCAGACTTAGCTGTGCCAG	183
Dd		21 IletnrcyBvAglAlaserGlnSerLeuValSerIleSerAmTyreunAlatPtyrGln	40
OY		184 CAGAAACCTGGCCAGGCTCCCAGGCTCTCATCTATGTGTCATCCACCAAGGCCACTGGC	243
Dd		41 GlnlySPROGilylAlaProllysleuenuIetYrAlalaserSerleugInseryly	60
OY		244 ATGCCAGACAGGTCAGTGGCAGTGGGAGTCCGGAGACAGACTTCACTCACCATCAGTAGA	303
Dd		61 ValProserArghPheSerylserylyserglyThrAspPheThrleuthrlleSerSer	80
OY		304 CTGAGAGCTGAAGATTTTGTCAGTGTATTACTGTACAGCAGTATGTAGCTCACCCTCAGACA	363
Dd		81 LeugInPProGIuaspPheAlathrYrYrCyvGInGIntYrAspSer-----Leu	97
OY		364 CCTGAGAGCTATTGGGCGGAGGAGCAAGAGTGGAGATCAAGAACGATCGGTGGTGACCA	423
Dd		98 ProGIutPhmrPheGlyGlnelylmrYsvAlGluIllelyGlySer-----	113
OY		424 TCTGTCTTGGCGGTGGCGGTTCGGAAGGTGGTGCATCAGGTGAGGTGGCTCCAGTGG	483
Dd		114 -----ThrserylySerylyLysPProGIyserylynglylserythrlyssglylval	131
OY		484 CAGCTGTGTGAGTCTTGGGGGAGGCGTGTGTCAGGCTGGGAGGTCTCTGAGACTCTCTGT	543
Dd		132 GlmleuValGlnuserylyGlylyeuValGlnPProGIyGlySerleuuarlguseryCyv	151
OY		544 GCAGGCTCTGGAATTCCTTCGAAGAGCTTTGGTATGCACTGGAGTCCGACAGGCTCAAGC	603
Dd		152 AlalaIsesrylyPheImrPheSerSerlyrAlametsertTPvalArGlnAlasPProGIy	171
OY		604 AAGGAGCTGAGTGGGTGGCAGTTATATCA-----TATGATGAAGACATAATTAATAC	657

|||||  
Db 172 LysGlyLeuGIuTrpValSerValIleSerGlyLysThrAspDlyGlySerThrTyr 191  
QY 658 GCAAGACTCGTGAAGGGCGGATTACCATCTCCAGAGACATTCCAAAGACGGTGAT 717  
Db 192 AlaAspSerValIleGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 211  
QY 718 CTAATAATGAACGCTTGAGAACTGAGACACGGCTGTATTAAGTGTGAGAGATCAG 777  
Db 212 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArgGlyArg 231  
QY 778 -----AGCTGTGGGTGACTATGACCACTACTACGCTTGAGCGTGGGGCAAA 828  
Db 232 \*\*\*Gly\*\*\*SerLeuSerGly\*\*\*TyrTyrTyrTyrHisTyrPheAspTyrTrpGlyGln 251  
QY 829 GGGACCAAGGTGACCGCTCTCTCAGAGATCCGAACAAA 867  
Db 252 GlyThrLeuValThrValSerSerLysLysLysLys 264  
RESULT 7  
US-09-983-580-6  
/ Sequence 6, Application US/09983580  
/ Patent No. 6764853  
/ GENERAL INFORMATION:  
/ APPLICANT: Filipula, David R.  
/ APPLICANT: Wang, Maoliang  
/ APPLICANT: Whitlow, Marc D.  
/ TITLE OF INVENTION: No. 6764853el Method for Targeted Delivery of Nucleic Acids  
/ FILE REFERENCE: 0977.2300002  
/ CURRENT APPLICATION NUMBER: US/09/983,580  
/ PRIOR FILING DATE: 2001-10-25  
/ PRIOR APPLICATION NUMBER: 09/420,592  
/ PRIOR FILING DATE: 1999-10-19  
/ PRIOR APPLICATION NUMBER: 60/104,949  
/ PRIOR FILING DATE: 1998-10-20  
/ NUMBER OF SEQ ID NOS: 13  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 6  
/ LENGTH: 283  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Kabat  
/ OTHER INFORMATION: Consensus  
/ NAME/KEY: UNSURE  
/ LOCATION: (232)  
/ OTHER INFORMATION: May be any amino acid.  
/ NAME/KEY: UNSURE  
/ LOCATION: (234)  
/ OTHER INFORMATION: May be any amino acid.  
/ NAME/KEY: UNSURE  
/ LOCATION: (239)  
/ OTHER INFORMATION: May be any amino acid.  
US-09-983-580-6  
Alignment Scores:  
Pred. No.: 5,71e-67 Length: 283  
Score: 892.00 Matches: 181  
Percent Similarity: 76.92% Conservative: 29  
Best Local Similarity: 66.30% Mismatches: 47  
Query Match: 52.07% Indels: 16  
DB: 4 Gaps: 5  
US-09-194-164-13 (1-918) x US-09-983-580-6 (1-283)  
QY 70 GATATTGTGTGACGAGCTCCAGGACCCGTGCTTTGCTCCAGGGAGAAAGACACC 129  
Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValAlaPheGlyValThr 20  
QY 130 CTCCTCGAGGGCGGACGATCAGAGTGT-----AGTAGACGACTTACCTTGGTGGTACG 183  
Db 21 IleThrCysArgAlaSerGlnSerLeuValSerIleSerAsnTyrLeuAlaTrpTyrGln 40

QY 184 CAGAACTGGCCAGGCTCCAGGCTCCTCATATGATGATCCAGCAGGCGCACTGAC 243  
Db 41 GlnLysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGly 60  
QY 244 ATGCCAGACAGTTTCAGTGGCGATGGTCCGGAGACAGACTTCACTTCATCAGTGA 303  
Db 61 ValProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSer 80  
QY 304 CTGAGCGCTGAAGATTTTGGAGTGTATTAAGTGTGAGAGATGATGATGATGATGATG 363  
Db 81 LeuGlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSer-----Leu 97  
QY 364 CCTCAGATCACTTTCGGCGAGGAGGACCAAGGTGAGATCAACAGACTGTGGCTGACCA 423  
Db 98 ProGluTrpThrPheGlyGlnGlyThrLysValGluIleLysGlySer----- 113  
QY 424 TCTGTCTCTGGCGGTGGCGGTTCGAGAGGTGGATGAGTGGAGGTGCTCCAGGTG 483  
Db 114 -----ThrSerGlySerGlyLysProGlySerGlyGlnGlySerThrLysGlyGlnVal 131  
QY 484 CAGCTGTGAGATCTGGGGGAGGCGCTGATCCAGCCTGGAGAGGTCCCTGAGACTCCTGT 543  
Db 132 GlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeuSerCys 151  
QY 544 GCAAGCTCGATTCCTCCCTCAGAGCTTGTGATGACTGGGTCCGCGAGGCTCTAGGC 603  
Db 152 AlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGlnAlaProGly 171  
QY 604 AAGGGCTGAGAGTGGGTGGCACTTATATCA-----TATGATGAAGCATTAATATCTAC 657  
Db 172 LysGlyLeuGIuTrpValSerValIleSerGlyLysThrAspGlyGlySerThrTyrTyr 191  
QY 658 GCAAGCTCGTGAAGGGCGGATTCACATCTCCAGACACTTCCAAAGACAGGATGAT 717  
Db 192 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 211  
QY 718 CTAATAATGAACGCTTGAGAACTGAGACACGGCTGTATTAAGTGTGAGAGATCAG 777  
Db 212 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArgGlyArg 231  
QY 778 -----AGCTGTGGGTGACTATGACCACTACTACGCTTGAGCGTGGGGCAAA 828  
Db 232 \*\*\*Gly\*\*\*SerLeuSerGly\*\*\*TyrTyrTyrTyrHisTyrPheAspTyrTrpGlyGln 251  
QY 829 GGGACCAAGGTGACCGCTCTCTCAGAGATCCGAACAAA 867  
Db 252 GlyThrLeuValThrValSerSerLysLysLysLys 264  
RESULT 8  
US-09-069-821-3  
/ Sequence 3, Application US/09069821  
/ Patent No. 6323322  
/ GENERAL INFORMATION:  
/ APPLICANT: FILIPULA, DAVID  
/ APPLICANT: WANG, MAOLIANG  
/ APPLICANT: SHORR, ROBERT  
/ APPLICANT: WHITLOW, MARC  
/ APPLICANT: LEE, LISHYNG S.  
/ TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
/ TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF  
/ NUMBER OF SEQUENCES: 33  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
/ STREET: 1100 NEW YORK AVE., NW, SUITE 600  
/ CITY: WASHINGTON  
/ STATE: DC  
/ COUNTRY: USA  
/ ZIP: 20005  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/069,821  
FILING DATE: 30-APR-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/067,341  
FILING DATE: 02-DEC-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH U.  
REGISTRATION NUMBER: 40,679  
REFERENCE/DOCKET NUMBER: 0977.2280003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-09-069-821-3

Alignment Scores:  
Pred. No.: 1,486-66 Length: 263  
Score: 887.00 Matches: 180  
Percent Similarity: 77.24% Conservative: 27  
Best Local Similarity: 67.16% Mismatches: 45  
Query Match: 51.78% Indels: 16  
Gaps: 5

US-09-194-164-13 (1-918) x US-09-069-821-3 (1-263)

QY 70 GATATTGTTGGAGCTTCACAGGACCCCTGTTCTCTCCAGGGGAAGACCCACC 129  
DB 1 AaplliegImetThrlserProserSerleuSerAlaSerValGlyAAspArgValThr 20  
QY 130 CTCTCCTGAGGCGCAGCTCAGAGTGT-----AGTAGAGCTACTTACCTGAGTACG 183  
DB 21 lIethrCyAArgAlaSerleuSerleuValSerlleSerAenThyleuAlaTrpIyrGln 40  
QY 184 CAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGTGATCCACAGGGCCACTGGC 243  
DB 41 GlnYsPProGlyLylAAlaProlysleuIleuIleTyAlaAlaSerSerleuGlnSerGly 60  
QY 244 ATGCAGACAGGTTGAGTGGGAGTGGGTCGGGAGACAGCTTCACCTCAGCTCAGTGA 303  
DB 61 ValProSerAArgPheSerleuSerleuSerGlyThrAAspPheThrleuThrIleSerSer 80  
QY 304 CTGAGCCTGAGATTTTGGAGTGTATTAAGTGTACAGAGTGTAGTCACTCAGACA 363  
DB 81 leuGlnPProGlnAAspPheAlaThrIyrIyrGylGlnGlnIleTyAAspSer-----Leu 97  
QY 364 CCTCAGATCCTTTGGGCGGAGGAGCAAGGTGAGATCAACGAACTGTGGTGCACCA 423  
DB 98 ProGlnTrpThrPheGlyGlnGlyThrIyrValGlnIleTyGlySer-----113  
QY 424 TCTGTCTGGGCGGAGTGGGTCGGGAGTGGTGTGATCAGCTGAGAGTGGCTCCAGGTG 483  
DB 114 -----ThrSerGlySerleuValAAspProGlySerGlyGlnGlySerThrIyrGlyGlnVal 131  
QY 484 CAGCTGTGAGTCTGGGCGGAGGCGTGTGTCAGCTGAGGAGGTCCCTGAGACTCTCCCTGT 543  
DB 132 GlnleuValGlnSerGlyGlyIleuValGlnPProGlyGlySerleuArgleuSerGly 151

QY 544 GGAGCTCTGATTCCTCCCTTACAGAACTTGTCTATGACTGGGTCGGCAGGCTTACGC 603  
DB 152 AlaAlaSerGlyPheThrPheSerSerIleuValMetSerTrpValArgGlnAlaProGly 171  
QY 604 AAGGGCTGAGTGGGTCAGTATATCA-----TATGATGAGAACTAAATACTAC 657  
DB 172 lYsGlyleuGlnTrpValSerValIleSerGlylYsThrAAspGlyGlySerThrIyr 191  
QY 658 GCAGACTCCGTGAAGGCGGATTCACCATCTCCAGAGACATTCACAGAGCGGTAT 717  
DB 192 AlaAspSerValIyrGlyAArgPheThrIleSerAArgAAspAAspSerIleuThrIleuTy 211  
QY 718 CTAATAATGACAGCTGAGAACTGAGACACAGGCTGTATTAATCTGTCCGAGATCAG 777  
DB 212 leuGlnMetAAspSerleuAArgAlaGlnAAspThrAlaValIyrIyrCyAAlaArgGlyArg 231  
QY 778 -----AGCCTGTGGGTGACTATGACCACTACTACAGTGTGGAGCTGGGCGCAA 828  
DB 232 \*\*\*Gly\*\*\*SerleuSerGly\*\*\*IyrIyrIyrIyrIyrIyrIyrIyrIyrIyrIyrIyr 251  
QY 829 GGAACACAGCTACCGCTCTCTCA 852  
DB 252 GlyThrleuValThrValSerSer 259

RESULT 9  
US-09-956-086-3  
Sequence 3, Application US/09956086  
Patent No. 6743896  
GENERAL INFORMATION:  
APPLICANT: FILIPULA, DAVID  
WANG, MAOLING  
SHORR, ROBERT  
WHITLOW, MARC  
LEE, LIHSYNG S.  
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,086  
FILING DATE: 20-SEP-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,821  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH U.  
REGISTRATION NUMBER: 40,679  
REFERENCE/DOCKET NUMBER: 0977.2280003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids

```

;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: No. 6743896 Relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-956-086-3

```

```

Alignment Scores:
Pred. No.: 1,486-66 Length: 263
Score: 887.00 Matches: 180
Percent Similarity: 77.24% Conservative: 27
Best Local Similarity: 67.16% Mismatches: 45
Query Match: 51.78% Indels: 16
DB: 4 Gaps: 5

```

```

US-09-194-164-13 (1-918) x US-09-956-086-3 (1-263)

```

```

QY 70 GATATTGTGTGAGCGAGTCTCCAGGACCCCTGTCTTTGCTCCAGGGAGAAAGCCACC 129
   ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 AspIleGlmMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
QY 130 CTCTCCTGAGGGCCAGTCAAGTGT-----AGTAGAGACTTACTTACCTGAGTACCA 183
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 IetHrCyArGAlaSerGlnSerLeuValSerIleSerAsnTyrlleuAlaTrpTyrGln 40
QY 184 CAGAAACTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGCCACTGGC 243
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 41 GlnTyProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGly 60
QY 244 AAGCCAGAGAGTTCAGTGGAGTGGAGTCCGGAGAGACTTCACTCACTCACTCACTA 303
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ValProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSer 80
QY 304 CTGAGACCTGAAGATTTTGCAGTGTATTACTGTCAACAGATGATGATCACTCACTCA 363
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 LeuGlnProGlnAspHeaIaThrTyrTyrCysGlnGlnTyrAsnSer-----Leu 97
QY 364 CCTCAGATCACTTGGCGGAGGAGGAGCCAGGTGAATCAAGAACTGGCTGCAGCA 423
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 98 ProGlnTrpThrPheGlnGlyGlnGlyThrLysValGlnIleLysGlySer----- 113
QY 424 TCTGCTCTGGCGGCGGCTCCGAGGAGTGTGATCAAGTGGAGGTGGCTCCAGGTG 483
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 114 -----ThSerGlySerGlyLysProGlySerGlyGlnGlySerThrLysGlyVal 131
QY 484 CAGCTGTGAGATCTGGGAGGAGCGTGTCAAGCTGGAGAGTCCCTGAGACTCTCTGT 543
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 132 GlnLeuValGlnSerGlyGlyGlyLeuValGlnProGlyLysLeuAlaGlnSerCys 151
QY 544 GCAGCTCTGAGATTCCTCCCTCAAGACTTTCATGACATCGGCTCCGCGAGGCTCA 603
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 152 AlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTyrValGlnAlaProGly 171
QY 604 AAGGAGCTGAGAGTGGGAGTGAATATCA-----TATGATGAAGACTTAATATCA 657
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 LysGlyLeuGlnTrpAlaSerValIleSerGlyLysThrAspGlySerThrTyrTyr 191
QY 658 GCAGACTCTCGTGAAGGCGCATTCACCATCTCCAGAGACATTCACAAAGACAGGTGAT 717
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 192 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 211
QY 718 CTAAATGAACGCTGAGAGACTGAGAGACAGGCTCTCTATTACTGTGGAGAGATCAG 777
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 212 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaAlaGlyArg 231
QY 778 -----AGCGCTGTGGTGAAGTATGACCACTACTACTGATTGAGCTGGGGGAA 828
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 ***Gly***SerLeuSerGly***TyrTyrTyrTyrHisTyrPheAspTyrTrpGlyGln 251
QY 829 GAGAGCAAGGTCAACCGTCTCTCA 852
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 252 GlyThrLeuValThrValSerSer 259

```

```

RESULT 10
US-09-956-087-3
; Sequence 3, Application US/09956087
; Patent No. 6743908
; GENERAL INFORMATION:
; APPLICANT: FILIPULA, DAVID
;           WANG, MAOLIANG
;           SHORR, ROBERT
;           WHITLOW, MARC
;           LEE, LISHYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSER: STERNF. KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,087
; FILING DATE: 20-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,821
; FILING DATE: 1998-04-30
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-Oct-1997
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-Jun-1997
; APPLICATION NUMBER: US 60/044,449
; FILING DATE: 30-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KIM, JUDITH U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 0977.2280003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-956-087-3
;
; Alignment Scores:
Pred. No.: 1,486-66 Length: 263
Score: 887.00 Matches: 180
Percent Similarity: 77.24% Conservative: 27
Best Local Similarity: 67.16% Mismatches: 45
Query Match: 51.78% Indels: 16
DB: 4 Gaps: 5
;
US-09-194-164-13 (1-918) x US-09-956-087-3 (1-263)
;
QY 70 GATATTGTGTGAGCGAGTCTCCAGGACCCCTGTCTTTGCTCCAGGGAGAAAGCCACC 129
   ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 AspIleGlmMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
QY 130 CTCTCCTGAGGGCCAGTCAAGTGT-----AGTAGAGACTTACTTACCTGAGTACCA 183
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 IetHrCyArGAlaSerGlnSerLeuValSerIleSerAsnTyrlleuAlaTrpTyrGln 40

```



Sequence 147, Application US/08488113B  
Patent No. 5744380  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studinka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF INVENTION: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-9155  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ. ID NO: 147:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-113B-147  
Alignment Scores:  
Pred. No.: 1,466-61 Length: 240  
Score: 827.50 Matches: 161  
Percent Similarity: 75.86 Conservative: 37  
Best Local Similarity: 61.69 Mismatches: 42  
Query Match: 48.31 Indels: 21  
DB: 1 Gaps: 5  
US-09-194-164-13 (1-918) x US-08-488-113B-147 (1-240)  
QY 70 GATATGTGTGCGAGCTCCAGGACCCCTTTGCTCCAGGAGAAAGCCACC 129  
DB 1 AapllleGlmethterInserProserSerleuSerValdlyaspArgValThr 20  
QY 130 CTCCTCGAGGCGGACGATGAGTGTAGTACGAGCTACTAGCTGATACAGCAGAA 189  
DB 21 lIethCyarArgAlaserInaspIle---AanSerTyIeuserTrpIhegIngnInys 39

QY 190 CTTGGCCAGGCTCCAGGCTCCTCATCTATGATGATCCACAGGCGCATGATGCA 249  
DB 40 ProgllylAlaProlyrThrleuIleTyrrArgAlaAnaArgleuIuSerIleValPro 59  
QY 250 GACAGGTCAGTGGAGGAGGTCGGGACAGACTTCACTTCACCATCAGTAGAGCTGAG 309  
DB 60 SerArgPheSerIleTyrrSerIleTyrrThrAspTyrrThrleuThrIleSerSerleuGln 79  
QY 310 CCGAAGATTTTGCAGTGTATTAAGTACAGCAGTATGAGTACCTCCTCAGACCTCAG 369  
DB 80 TyrrGluAapPhegllyIleTyrrTyrrCysGlnGlnTyrrAspGluSerProTrp----- 96  
QY 370 ATCACTTCGGGAGGAGGACCAAGGTGAGATCAACAGCACTGTGCTGACCATCTGTC 429  
DB 97 ---ThrPhegllylgllylThrlybLeuGlnUweIys----- 107  
QY 430 TCTGGCGGTGGCGGTTCCGAGGTGTGATCAGGTGAGGTGCTCCAGGTGACGCTG 489  
DB 108 ---GlygllylgllylserGlygllylgllylserGlygllylgllylserGlnIleGlnleu 126  
QY 490 GTGAGTCTGGGGAGGCGGTGTGCTCCAGGAGCTCCAGACTCTCTCTGTGACGCC 549  
DB 127 ValGlnSerIlygllylgllyleuVallybProgllylserValArgIleSerCysAlaIa 146  
QY 550 TCTGATTCCTCCAGAAAGCTTGTGCTATGCACTGAGCTCCGCGAGGCTCTAGCAAGGG 609  
DB 147 SerGlyTyrrThrPheThrAsnTyrrIleYmeAsnTrpValArgGlnAlaProgllylser 166  
QY 610 CTGAGGTGGTGGCGAGTTATATCATATGATGAGAACATAATACAGCACTCCGTG 669  
DB 167 LeuGlnTrpMetGlyTrpIleAsnThrHisThrGlyGlnProThrTyrrAlaAspSerPhe 186  
QY 670 AAGGCCCATTCACCATCTCCAGAGACTTCCAAAGAACAGGTTATCTAAATGAAAC 729  
DB 187 LysGlyArgPheThrPheSerleuAspSerIysAsnThrAlaTyrrleuGlnIleAsn 206  
QY 730 AGCCTGAGACTGAGGAGCAGCGGTGTATTAAGTGTGAGATCAGAGCTGTGGGT 789  
DB 207 SerleuAlaGlnAlaAspThrAlaValTyrrPheCysThrArg-----Arg 221  
QY 790 GACTATGACCACTACTACGAGTGTGGAGCTGTGGGCAAGGAGCAGGTCACCGTCC 849  
DB 222 GlyTyrrAspTrpTyrrPhe-----AspValTrpGlyGlnGlyThrThrValThrValSer 239  
QY 850 TCA 852  
DB 240 Ser 240  
RESULT 13  
US-08-477-484B-147  
Sequence 147, Application US/08477484B  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studinka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF INVENTION: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,484B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 147:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-484B-147

Alignment Scores:  
Pred. No.: 1,466-61 Length: 240  
Score: 827.50 Matches: 161  
Percent Similarity: 75.86% Conservative: 37  
Best Local Similarity: 41.69% Mismatches: 42  
Query Match: 48.31% Indels: 21  
DB: 1 Gaps: 5

US-09-194-164-13 (1-918) x US-08-477-484B-147 (1-240)

QY 70 GATATGTTGTTGACGAGCTCTCCAGGACCCCTGTTCTTCTCCAGGGGAAAGACCAACC 129  
DB 1 AapilegImetThrlnserProserSerleuSerAlaSerValGlyAspArgValThr 20  
QY 130 CTCCTCTGAGGGCCAGTGAAGTGTAGTACGACGCTTACTGCTGCTGACGACGAGAA 189  
DB 21 IlettrCYsArgAlaSerGlnAspIle--AenSerTYrLeuSerTrpPheGlnGlnYs 39  
QY 190 CTTGSCCAGGCTCCAGGCTCTCATCTATGTTGATCCACAGGAGGCCACCTGGCAGTCCA 249  
DB 40 ProGlyLysAlaProLysThrLeuIleTYrArgAlaAlaArgLeuGluSerGlyValPro 59  
QY 250 GACAGGTTCACTGAGGAGTGGCTCCGAGACAGACTTCACTCACTCACTCACTCACTGAG 309  
DB 60 SerArgPheSerGlySerGlySerGlyThrAspTYrThrLeuThrIleSerSerLeuGln 79  
QY 310 CCTGAAGATTTTGACGTGATTAATCTGTCAGCAGTATGTAAGTCACTCACTCACTCACT 369  
DB 80 TYrGluAspPheGlyIleTYrTYrCYsGlnGlnTYrAspGluSerProTrp----- 96  
QY 370 ATCACTTCGCGGAGGAGCAAGGTTGAGATCAACAGAACTGTGGCTGACATCTGTGC 429  
DB 97 ---ThrpheGlyGlyGlyThrylsLeuGluMetLys----- 107  
QY 430 TCTGCGGTTGGCGGTTCCGAGGCTGTGATCAGGTTGAGTGGCTCCGAGGTGACGCTG 489  
DB 108 ---GlyGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlyGlySerGlnIleGlnLeu 126  
QY 490 GTGAGAGTCTGGGGAGGCGCTGTCCAGCTGTGGAGAGTCCCTGAGACTCTCTGTGTGACGC 549

DB 127 ValGlnSerGlyGlyGlyLeuValLysProGlyGlySerValArgIleSerCysAlaAla 146  
QY 550 TCTGATTCCTCCCTTGAAGCTTTGCTATGACCTGGGTCCGAGGCTTCAAGCAAGGG 609  
DB 147 SerGlyTYrThrPheThrAsnTYrGlyMetLeuThrValArgGlnAlaProGlyGly 166  
QY 610 CTGAGGTGGGTGGCAGTTATATCATATGATGAGACCACTAAATCTACGACGACTCCGG 669  
DB 167 LeuGluTrpMetGlyTrpIleAsnThrIleAsnThrGlyGluProThrTYrIleAspSerPhe 186  
QY 670 AAGGCGCATTCACATCTCCAGACACTTCCAGAGACAGCGGTATTAATAATGANC 729  
DB 187 LysGlyArgPheThrPheSerLeuAspAspSerLysAsnThrAlaTYrLeuGlnIleAsn 206  
QY 730 AGCTGAGAACTGAGACAGCGCTGTCTATTACTGTGCGAGAGATCAGAGCCTGTGGGT 789  
DB 207 SerLeuArgAlaGluAspThrAlaValTYrPheCYsThrArg-----Arg 221  
QY 790 GACTATGACCACTACTACGCTTTGACGCTCTGGGCGAAAGGACCAAGGCTCACTGCTCC 849  
DB 222 GlyTYrAspTrpTYrPhe-----AspValTrpGlyGlnGlyTYrThrValThrValSer 239  
QY 850 TCA 852  
DB 240 Ser 240

RESULT 14  
US-08-646-360-147  
Sequence 147 Application US/08646360  
Patent No. 5837491  
GENERAL INFORMATION:  
APPLICANT: Belter, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSER: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4

```
TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 147:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 240 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-646-360-147

Alignment Scores:
Pred. No.: 1,46e-61 Length: 240
Score: 827.50 Matches: 161
Percent Similarity: 75.86% Conservative: 37
Best Local Similarity: 61.69% Mismatches: 42
Query Match: 48.31% Indels: 21
DB: 2 Gaps: 5

US-09-194-164-13 (1-918) x US-08-646-360-147 (1-240)
QY 70 GATATTGTGTGACGACGCTCCAGGACCCCTGTTGTCACAGGAGAAAGCCACC 129
Db 1 AsplleqlmMetThrglnSerProSerSerleuSerAlaSerValglAapArgValThr 20
QY 130 CTCGCCGACGAGGCGCATGCTAGAGTTAGACGCTACTTACCTGCTGACGAGAAA 189
Db 21 lIethrcyAargAlaSerGlnAaple--AasbertyleuSertrpPheGlnGlnlys 39
QY 190 CTTGGCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGCGCATGCGCATGCCA 249
Db 40 ProgllysalAlaProlysthrleuIleTyraAlaAsnArgleuIuSerGlyValPro 59
QY 250 GACAGGTTCTGTCGTCAGTGGCTCCGAGACACTTCACTTCCATCAGTAGACTGAG 309
Db 60 SerArgheserGlyserGlyserGlyThrAspTyrThrleuThrIleSerSerleuGln 79
QY 310 CTTGAAGATTGTCAGTATTAAGTGTGACAGTATGATGATGATGATGATGATGATG 369
Db 80 TyrglAasPheGlyIleTyrrTCySglnGlnIlyAspGluSerProTrp----- 96
QY 370 ATCACTTTCGCGGAGGAGCAAGGATGAGATCAAAAGATGTCGCTGACCATCTGTC 429
Db 97 ---ThrphegllygllyThrlyleuGlnMetlys----- 107
QY 430 TCTGGGGGTGGCGGTTCCGAGGTGTGATCAGGTGAGAGTGGCTCCAGGTGACGCTG 489
Db 108 --GlygllygllygllyserGlygllygllyserGlygllygllygllyserGlnleu 126
QY 490 GTGAGATCTGGGAGGAGCGTGTCCAGGCTGGGAGGCTCCGAGTCTCTGTCGAGGC 549
Db 127 ValGlnSerGlygllygllyleuVallyspGroglygllySerValArgIleSerGlyAla 146
QY 550 TCTGATTCCTCTTCAAGACTTGTGATGACCTGAGGCTCCGAGGCTTGAAGCAAGG 609
Db 147 SerGlyTyrThrPheThrSerIleuTyrglyMetAlaSerTrpValArgGlnAlaProglylysgly 166
QY 610 CTGGAGTGGGTGGCAGTTATATCATATGATGAGAGCACTAAATACGACAGTCCGCG 669
Db 167 LeuGlnIrrpMetGlyTrpIleleuThrHsthnglygluProThrTyrAlaAspSerPhe 186
QY 670 AAGGGCCGATTCACTTCACAGACACTTCCAGAGACAGGATGATCTTAAATAAAGAAC 729
Db 187 LysgllyArgPheThrPheSerleuAspAspSerlyAsnThrAlaTyrlleuGlnIleAsn 206
QY 730 AGCTTAGAAGTGAAGACAGCGGTGTCTATTAAGTGTGCAAGAGATCAAGACCTGTTGG 789
Db 207 SerleuArgAlaGlnAspThrAlaValTyrrPheCyThrArg-----Arg 221
QY 790 GACTATGACACACTACGATGATTGAGCGTCTGGGGCAAGGAGACACAGGTCAACGCTTCC 849
Db 222 GlyTyrAspTrpTyrPhe-----AspValIrrpGlyGlnGlyThrThrValThrValSer 239
```

```
QY 850 TCA 852
Db 240 Ser 240

RESULT 15
US-08-839-765-147
/ Sequence 147, Application US/08839765
/ Patent No. 614631
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Studika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ TITLE OF INVENTION: Proteins
/ NUMBER OF SEQUENCES: 169
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSER: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentln Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/839,765
/ FILING DATE: 15-APR-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-9155
/ TELEFAX: 312/707-8889
/ INFORMATION FOR SEQ ID NO: 147:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 240 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-839-765-147

Alignment Scores:
Pred. No.: 1,46e-61 Length: 240
Score: 827.50 Matches: 161
Percent Similarity: 75.86% Conservative: 37
Best Local Similarity: 61.69% Mismatches: 42
Query Match: 48.31% Indels: 21
DB: 3 Gaps: 5

US-09-194-164-13 (1-918) x US-08-839-765-147 (1-240)
```





**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 18, 2005, 08:38:58 ; Search time 203 Seconds  
(without alignments)  
2959.678 Million cell updates/sec

Title: US-09-194-164-13

Perfect score: 1713  
Sequence: 1 GAATTCATGAAAAAAGCGC.....ATCACCATTAGTGAAGCTT 918

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1380268 seqs, 327241040 residues  
Total number of hits satisfying chosen parameters: 2760536

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame-n2p.model -DEV=xlh  
-O=/cgn2\_1/USPTO\_epool/US09194164/runat\_16022005\_122614\_6076/app\_query.fasta\_1.1095  
-DB=Published Applications AA -CPMT=faetan -SUFFIX=xapb -MINMATCH=0.1  
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USR=US09194164\_@CGN\_1\_1\_86\_@runat\_16022005\_122614\_6076  
-NCPV=6 -ICPV=3 -NO MMAP -LARGEOQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	1573	91.8	304	10	US-09-782-397-14	Sequence 14, Appl
2	1573	91.8	304	15	US-10-651-453-14	Sequence 14, Appl
3	1451.5	84.7	287	10	US-09-782-397-17	Sequence 17, Appl
4	1451.5	84.7	287	15	US-10-651-453-17	Sequence 17, Appl
5	928	54.2	352	10	US-09-203-958A-2	Sequence 2, Appl
6	926.5	54.1	456	15	US-10-634-862-11	Sequence 11, Appl
7	892	52.1	283	9	US-09-983-580-6	Sequence 6, Appl
8	892	52.1	283	9	US-09-983-580-6	Sequence 6, Appl
9	887	51.8	263	9	US-09-956-086-3	Sequence 3, Appl
10	887	51.8	263	9	US-09-956-086-3	Sequence 3, Appl
11	866.5	50.6	630	15	US-10-422-628-18	Sequence 48, Appl
12	866.5	50.6	630	15	US-10-422-628-18	Sequence 16, Appl
13	863.5	50.4	277	15	US-10-422-628-16	Sequence 43, Appl
14	857.5	50.1	279	15	US-10-409-938-21	Sequence 21, Appl
15	849.5	49.6	252	15	US-10-423-847-10	Sequence 10, Appl
16	849.5	49.6	252	15	US-10-423-847-14	Sequence 14, Appl
17	849.5	49.6	253	15	US-10-423-847-11	Sequence 11, Appl
18	849.5	49.6	254	15	US-10-423-847-17	Sequence 17, Appl
19	847	49.4	239	15	US-10-423-847-18	Sequence 18, Appl
20	827.5	48.3	240	14	US-10-127-890-147	Sequence 147, Appl
21	824.5	48.1	247	15	US-10-423-847-13	Sequence 13, Appl
22	824	48.1	443	13	US-10-006-773-2	Sequence 2, Appl
23	824	48.1	443	13	US-10-006-773A-2	Sequence 2, Appl
24	810	47.3	4852	15	US-10-412-406-33	Sequence 33, Appl
25	808.5	47.2	409	15	US-10-353-121-21	Sequence 14, Appl
26	807.5	47.1	502	16	US-10-679-620-88	Sequence 88, Appl
27	806.5	47.1	663	15	US-10-412-406-32	Sequence 32, Appl
28	805	47.0	408	15	US-10-353-721-15	Sequence 15, Appl
29	803.5	46.9	252	9	US-09-971-543-1	Sequence 1, Appl
30	784.5	45.8	364	16	US-10-829-388-11	Sequence 11, Appl
31	784.5	45.8	370	16	US-10-829-388-1	Sequence 1, Appl
32	784	45.8	271	10	US-09-226-157-4	Sequence 4, Appl
33	784	45.8	374	14	US-10-335-394-15	Sequence 15, Appl
34	779.5	45.5	491	13	US-10-011-125-2	Sequence 2, Appl
35	777.5	45.4	543	14	US-10-207-655-146	Sequence 146, Appl
36	773	45.1	556	14	US-10-207-655-268	Sequence 268, Appl
37	770	45.0	256	15	US-10-418-182-2	Sequence 2, Appl
38	769.5	44.9	492	14	US-10-207-655-344	Sequence 344, Appl
39	767.5	44.8	543	14	US-10-207-655-345	Sequence 345, Appl
40	766	44.7	298	9	US-09-883-758-2	Sequence 2, Appl
41	762.5	44.5	431	14	US-10-013-173-4	Sequence 4, Appl
42	762.5	44.5	431	14	US-10-150-762-4	Sequence 4, Appl
43	762.5	44.5	431	14	US-10-244-821-4	Sequence 4, Appl
44	761	44.4	258	14	US-10-207-655-343	Sequence 343, Appl
45	759.5	44.3	271	14	US-10-207-655-254	Sequence 254, Appl

## ALIGNMENTS

RESULT 1  
US-09-782-397-14  
; Sequence 14, Application US/09782397  
; Publication No. US20030021779A1  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
Kaplan, Pradipt K.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
SPECIFICALLY DIRECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 304 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-782-397-14

Alignment Scores:  
Pred. No.: 1,93e-103 Length: 304  
Score: 1573.00 Matches: 302  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 91.83% Indels: 0  
DB: 10 Gaps: 0

US-09-194-164-13 (1-918) x US-09-782-397-14 (1-304)

QY 1 GAATTCATGAAAAAACCCTATCGCATGCGAGTGGCTGTTGGCTACCGTT 60  
DB 1 GluPheMetLysIsthrAlaIleAlaValAlaLeuAlaGlyPheAlaThrVal 20  
QY 61 GCCGAGCCGATATGTGTGACGCGAGTCTCCAGGACCCCTGTTCTCCAGGGGAA 120  
DB 21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGlu 40  
QY 121 AGAGCCACCCCTCCCGGAGGGCGAGTCAAGTGTAGTAAAGCGTAACTTACCTGTAC 180  
DB 41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerTyrLeuAlaTrpTyr 60  
QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATGTATGATGCATCCAGGGGCGACT 240  
DB 61 GlnGlnLysProGlyGlnAlaProArgLeuLeuIleTyrGlyAlaSerThrArgAlaThr 80  
QY 241 GCGATGCCAGACGAGTTCAGTGGAGTGGGTCGGGACAGACTTCACTCCATCACTCACT 300  
DB 81 GlyMetProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer 100  
QY 301 AGACTGAGCGCTGAATTTTGCAGGTATTACTGTCCACAGATAGTGTAGCTCACTCG 360  
DB 101 ArgLeuGlnProGlnAspPheAlaValTyrCysGlnGlnIleTyrGlySerSerProGln 120  
QY 361 ACACTCAGATCACTTTCGCGAGGAGCAACAGTGGAGATCAACGAACTGTGGCTGCA 420  
DB 121 ThrProGlnIleThrPheGlyGlyGlyThrLysValGlnIleLysArgThrAlaAla 140  
QY 421 CCATCTGTCTTGGCGGTGGCGGTTCCGAGGTGGTGAATCAAGTGGAGTGGCTCCAG 480  
DB 141 ProSerValSerGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlySerGln 160  
QY 481 GTGCACTGTGTGAGTCTGGGGAGGCGGTCCAGGCGGGAGGCTCCGAGATTCCTCC 540  
DB 161 ValGlnLeuValGlnSerGlyGlyGlyValValGlnProGlyArgSerLeuArgLeuSer 180

QY 541 TGTGACGCTTTCGATTCCTCCCTTCAGAACCTTTGCTATGACTGGGTCCGCGAGCTCTA 600  
DB 181 CysAlaAlaSerGlyPheProPheArgSerPheAlaMetHisTrpValArgGlnAlaLeu 200  
QY 601 GCGAAGGGGCTGAGAGTGGGTGGCAGTTATATATATGATGGAAGACTAAATATACGCA 660  
DB 201 GlyLysGlyLeuGlnIleThrValAlaValIleSerTyrAspGlySerThrLysTyrTrpAla 220  
QY 661 GACTCGGTGAAGGCGCATTCACCATCTCCAGAGACACTTCCAGAAACAGGTGTATCTA 720  
DB 221 AspSerValLysGlyArgPheThrIleSerArgAspThrSerLysAsnThrValTyrLeu 240  
QY 721 AAAATGACAGGCTGAGAACTAGAGACACGCGTGTCTATTACTGTCCAGAGATCAGAC 780  
DB 241 LysMetAsnSerLeuArgThrGlnAspThrAlaValTyrCysAlaArgAspGlnSer 260  
QY 781 CTGTTGGGTGACTATGACCACTACACGTTTGTGAGCTGGGGGCAAGGACACGCGTC 840  
DB 261 LeuLeuGlyAspTyrAspHisTyrTyrGlyLeuAspValIleProGlyLysGlyThrThrVal 280  
QY 841 ACCGTCTCTCGAGATCCGAACAAACTGATCAGCGAAGAGATCTGAACCATCAGCAT 900  
DB 281 ThrValSerSerGlySerGlyGlnLysLeuIleSerGlnGlnAspLeuAsnHisHis 300  
QY 901 CACCAT 906  
DB 301 HisHis 302

## RESULT 2

US-10-651-453-14

Sequence 14, Application US/10651453

Publication No. US20040091484A1

GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

APPLICANT: Matli, Pradipt K.

APPLICANT: Kaplan, Howard A.

TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PRO

TITLE OF INVENTION: DETECTION OF CANCERS

FILE REFERENCE: 316082000103

CURRENT APPLICATION NUMBER: US/10/651, 453

CURRENT FILING DATE: 2003-08-29

PRIOR APPLICATION NUMBER: US 09/782,397

PRIOR FILING DATE: 2001-02-13

PRIOR APPLICATION NUMBER: US 08/862,124

PRIOR FILING DATE: 1997-05-22

PRIOR APPLICATION NUMBER: US 08/657,449

PRIOR FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn version 3.1

SEQ ID NO 14

LENGTH: 304

TYPE: PRT

ORGANISM: Homo Sapiens

US-10-651-453-14

## Alignment Scores:

Pred. No.: 1,93e-103 Length: 304  
Score: 1573.00 Matches: 302  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 91.83% Indels: 0  
DB: 15 Gaps: 0

US-09-194-164-13 (1-918) x US-10-651-453-14 (1-304)

QY 1 GAATTCATGAAAAAACCCTATCGCATGCGAGTGGCTGTTGGCTACCGTT 60  
DB 1 GluPheMetLysIsthrAlaIleAlaValAlaLeuAlaGlyPheAlaThrVal 20  
QY 61 GCCGAGCCGATATGTGTGACGCGAGTCTCCAGGACCCCTGTTCTCCAGGGGAA 120  
DB 21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGlu 40

121 AGAGCACCTCTCCGAGGCGCAGTCAAGTGTATAGCAGCTACTTACCTGTAC 180  
41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerCysLeuAlaTrpTyr 60  
181 CAGCAAAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTAGTACCAAGGCGCACT 240  
61 GlnGlnLysProGlnArgAlaProArgLeuLeuIleTyrGlyAlaSerThrArgAlaThr 80  
241 GGCATGCCAGACAGTTCAGTGGCAGTGGGTCGCGAGCAAGACTTCACTTCAACCATCACT 300  
81 GlyMetProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer 100  
301 AGACTGAGACCTGGAAGATTTTGCAGTGTATTACTGTCAGCAGTATAGTATAGTCACTCG 360  
101 ArgLeuGlnLysProGlnAspPheAlaValTyrTyrCysGlnGlnIleTyrGlySerSerProGln 120  
361 ACACCTCAGATCACTTTCGCGGAGGAGCAAGGTGAGATCAACGAAGTGGGTGCA 420  
121 ThrProGlnIleThrPheGlyGlyTyrLysValGlnIleLysArgThrValAlaAla 140  
421 CCATCTGTCTCTGCGCGTGGCGGCTTCGAGAGTGTGTGATCAGTGGAGTGGCTCCAG 480  
141 ProSerValSerGlyGlyGlySerGlyGlyGlySerGlyGlySerGlyGlySerGln 160  
481 GTGCGAGCTGTGAGTCTGGGGGAGCGCTGCTCAGCTCGGAGGTCCCTGAGACTCTCC 540  
161 ValGlnLeuValGlnSerGlyGlyGlyValAlaGlnProGlyArgSerLeuArgLeuSer 180  
541 TGTGAGACCTCTGATTCCTCCCTTCAAGAGCTTGTGATGACCTGGGTCCGCGAGCTCTA 600  
181 CysAlaAlaIleSerGlyPheProPheArgSerPheAlaMetHisTrpAlaArgGlnAlaLeu 200  
601 GCGAAGGGGCTGAGTGGGTGCGAGTATATCATATGATGAGAGCACTAAATATCAACGA 660  
201 GlyLysGlyLeuGlnLysValAlaValIleSerTyrAspGlySerThrLysTyrAla 220  
661 GACTCCGCGAAGGGCGGATTCACCATCTTCAGAGACACTTCCAAAGAACCGGTGATCTTA 720  
221 AspSerValLysGlyArgPheThrIleSerArgAspThrSerLysAsnThrValTyrLeu 240  
721 AAAATGAACAGCGCTGAGAACTGAGGACAGCGCTGTATTACTGTGCGGAGATCAAGGC 780  
241 LysMetAsnSerLeuArgThrGlnAspThrAlaValTyrTyrCysAlaArgAspGlnSer 260  
781 CTGTGTGATGATGACCACTACTACTACGTTTGAAGCTCTGGGCAAGGAGCAACGCTC 840  
261 LeuLeuGlyAspTyrAspIleTyrTyrGlyLeuAspValTrpGlyLysGlyThrThrVal 280  
841 ACCGTCCTCTCAGATCCGAAACAAAATGATCAGGGAAGAAAGATCTGAACCATCAACAT 900  
281 ThrValSerSerGlySerGlnGlnLysLeuIleSerGlnGlnAspLeuAsnHisHisHis 300  
901 CACCAT 906  
301 HisHis 302

RESULT 3  
US-09-782-397-17  
Sequence 17, Application US/09782397  
Publication No. US20030021779A1  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
Maitl, Pradipt K.  
Kaplan, Howard A.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road

CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,397  
FILING DATE: 13-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/862,124  
FILING DATE: 1997-05-22  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 287 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-782-397-17  
Alignment Scores:  
Pred. No.: 8-12e-95 Length: 287  
Score: 1451.50 Matches: 283  
Percent Similarity: 93.71% Conservative: 0  
Best Local Similarity: 93.71% Mismatches: 2  
Query Match: 84.73% Indels: 17  
Gaps: 1  
US-09-194-164-13 (1-918) x US-09-782-397-17 (1-287)  
QY 1 GAATTCAGAAAACCGCTATCGCATGCGAGTTCAGTGGCTTCCCTACCGTT 60  
DB 1 GlnPheMetCysLysThrAlaIleAlaValAlaLeuAlaGlyPheAlaThrVal 20  
QY 61 GCGCAGGCGCATATGTGTTGACAGCATCTCCAGGCAACCTGTTGCTCCAGGGGA 120  
DB 21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln 40  
QY 121 AGAGCACCTCTCTCGAGGCGCAGTCAAGTGTATAGTACGAGCTACTTACCTGTAC 180  
DB 41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerSerCysLeuAlaTrpTyr 60  
QY 181 CAGCAAAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTAGTACCAAGGCGCACT 240  
DB 61 GlnGlnLysProGlnArgAlaProArgLeuLeuIleTyrGlyAlaSerThrArgAlaThr 80  
QY 241 GGCATGCCAGACAGTTCAGTGGCAGTGGGTCGCGAGCAAGACTTCACTTCAACCATCACT 300  
DB 81 GlyMetProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer 100  
QY 301 AGACTGAGACCTGGAAGATTTTGCAGTGTATTACTGTCAGCAGTATAGTCACTCG 360  
DB 101 ArgLeuGlnLysProGlnAspPheAlaValTyrTyrCysGlnGlnIleTyrGlySerSerProGln 120  
QY 361 ACACCTCAGATCACTTTCGCGGAGGAGCAAGGTGAGATCAACGAAGTGGGTGCA 420  
DB 121 ThrProGlnIleThrPheGlyGlyTyrLysValGlnIleLysArgThrValAlaAla 140  
QY 421 CCATCTGTCTCTGCGCGTGGCGGCTTCGAGAGTGTGTGATCAGTGGAGTGGCTCCAG 480

```
Db 141 -----SerGlyGln 143
QY 481 GTGCAGCTGTGAGTCTGGGGGAGGCGTGTCCAGCCTTGCTCCAGACTCTCC 540
Db 144 ValGlnLeuValGlySerGlyGlyValGlnProGlyArgSerLeuArgLeuSer 163
QY 541 TGTGCAAGCGCTGTGATTCCTCCAGAACCTTGTATGACATCGGCTCCGACAGCTCTA 600
Db 164 CysAlaAlaSerGlyPheProPheArgSerPheAlaMetHisTrpAlaArgGlnAlaLeu 183
QY 601 GCCAAGAGGCGTGGAGTGGGCACTTATATCATATGATGAGACCTAATAATACACGA 660
Db 184 GlyIysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerThrIysTyrAla 203
QY 661 GACTCGTGAAGGCGGATTCACCATCTCCAGACACTTCCAGAACCGGTATCTTA 720
Db 204 AspSerValIysGlyArgPheThrIleSerArgAspThrSerIysAsnThrValTyrLeu 223
QY 721 AAAATGAACAGCTGGAACCTGAGACAGGCGTGTATTACTGTGGGAGAGATCAGAGC 780
Db 224 LysMetAsnSerLeuArgThrGluAspThrAlaValTyrTyrCysAlaArgAspGlnSer 243
QY 781 CTGTGGGTGACATGACCACTACTACGGTTTGGACGTGGGGCAAGGACCAAGCTGC 840
Db 244 LeuLeuGlyAspTyrAspHisTyrTyrGlyLeuAspValTyrGlyIysGlyThrVal 263
QY 841 ACCGTCCTCTCAGATCCGAAACAAAACCTGATCAGCGAAGAGATCTGAACCATCACCAT 900
Db 264 ThrValSerSerGlySerGlnGlnIysLeuIleSerGlnIysAspLeuAsnHisHis 283
QY 901 CACCAT 906
Db 284 HisHis 285

RESULT 4
US-10-651-453-17
; Sequence 17, Application US/10651453
; Publication No. US20040091484A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Mafti, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS.
; TITLE OF INVENTION: DETECTION OF CANCERS
; FILE REFERENCE: 316082000103
; CURRENT APPLICATION NUMBER: US/10/651,453
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 09/782,397
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 08/862,124
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: US 08/657,449
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-651-453-17

Alignment Scores:
Pred. No.: 8,12e-95 Length: 287
Score: 1451.50 Matches: 283
Percent Similarity: 93.71% Conservative: 0
Best Local Similarity: 93.71% Mismatches: 2
Query Match: 84.73% Indels: 17
DB: 15 Gaps: 1

US-09-194-164-13 (1-918) x US-10-651-453-17 (1-287)
QY 1 GAATTGATGAAAAAACCGCTATCGGATCGCAGTTGCACTGGCTGTTTCGCTACCGTT 60
```

```
Db 1 GluPheMetLysIysThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrVal 20
QY 61 GCGCAGCGCGATATTGTTGTTGACGCAAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGAA 120
Db 21 AlaGlnAlaAspIleValLeuThrGlnSerProGlyThrLeuSerLeuSerProGlyGln 40
QY 121 AGAGCCACCTCTCCGTGAGGGCCAGTCAAGTGTGTTAGTCAAGCTACTTACCGCTGTAC 180
Db 41 ArgAlaThrLeuSerCysArgAlaSerGlnSerValSerSerTyrLeuAlaTrpTyr 60
QY 181 CAGCAAAACCTGGGCGCAGGCTCCAGGCTCTCATATATGATGATCCACCAAGGCGCACT 240
Db 61 GlnGlnIysProGlyGlnAlaProArgLeuLeuIleTyrGlyAlaSerThrArgAlaThr 80
QY 241 GGCATGCCAAGACAGTTCAAGTGGCAGTGGGTCCGGAACAGACTTCACTCACTCACTAGT 300
Db 81 GlyMetProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer 100
QY 301 AGACTGAGCCTGGAAGATTTTGGCAGTATTAATGTCAGAGTATGTAAGCTCACTCAG 360
Db 101 ArgLeuGlnProGluAspPheAlaValTyrTyrCysGlnGlnTyrGlySerSerProGln 120
QY 361 ACACCTCAGATCACTTTCGGCGGAGGACCAAGGTGAGATCAACGAACCTGTGGCTGCA 420
Db 121 ThrProGlnIleThrPheGlyGlyGlyThrIysValGlnIleIysArgThrValAlaAla 140
QY 421 CCATCTGTCTCTGGCGGTGGCGGTTCCGAGGTGTGATCAGGTGAGGTGGCTCCAG 480
Db 141 -----SerGlyGln 143

QY 481 GTGCAGCTGTGAGTCTGGGGGAGGCGTGTCCAGCCTGGGAGGCTCCAGACTCTCC 540
Db 144 ValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeuSer 163
QY 541 TGTGCAAGCGCTGTGATTCCTCCAGAACCTTGTATGACATCGGCTCCGACAGCTCTA 600
Db 164 CysAlaAlaSerGlyPheProPheArgSerPheAlaMetHisTrpValArgGlnAlaLeu 183
QY 601 GCCAAGAGGCGTGGAGTGGGCACTTATATCATATGATGAGACCTAATAATACACCA 660
Db 184 GlyIysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerThrIysTyrAla 203
QY 661 GACTCGTGAAGGCGGATTCACCATCTCCAGACACTTCCAGAACCGGTATCTTA 720
Db 204 AspSerValIysGlyArgPheThrIleSerArgAspThrSerIysAsnThrValTyrLeu 223
QY 721 AAAATGAACAGCTGGAACCTGAGACAGGCGTGTATTACTGTGCGAGAGATCAGAGC 780
Db 224 LysMetAsnSerLeuArgThrGluAspThrAlaValTyrTyrCysAlaArgAspGlnSer 243
QY 781 CTGTGGGTGACATGACCACTACTACGGTTTGGACGTGGGGCAAGGACCAAGCTGC 840
Db 244 LeuLeuGlyAspTyrAspHisTyrTyrGlyLeuAspValTyrGlyIysGlyThrVal 263
QY 841 ACCGTCCTCTCAGATCCGAAACAAAACCTGATCAGCGAAGAGATCTGAACCATCACCAT 900
Db 264 ThrValSerSerGlySerGlnGlnIysLeuIleSerGlnIysAspLeuAsnHisHis 283
QY 901 CACCAT 906
Db 284 HisHis 285

RESULT 5
US-09-203-958A-2
; Sequence 2, Application US/09203958A
; Publication No. US20030039641A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: GOLDSTEIN, Joel
; APPLICANT: GRAZIANO, Robert
; APPLICANT: DEO, Yashwant M.
; TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR
```

```

/ TITLE OF INVENTION: BINDING COMPONENTS
/ FILE REFERENCE: MXI-099CPA
/ CURRENT APPLICATION NUMBER: US/09/203,958A
/ CURRENT FILING DATE: 1998-12-02
/ PRIOR APPLICATION NUMBER: 60/067232
/ PRIOR FILING DATE: 1997-12-02
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PasteSeq for Windows Version 4.0
/ SEQ ID NO: 2
/ LENGTH: 352
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
US-09-203-958A-2

Alignment Scores:
Pred. No.: 1,2e-57 Length: 352
Score: 928.00 Matches: 192
Percent Similarity: 75.438 Conservative: 26
Best Local Similarity: 66.448 Mismatches: 45
Query Match: 54.174 Indels: 26
DB: 10 Gaps: 5

US-09-194-164-13 (1-918) x US-09-203-958A-2 (1-352)
QY 52 GCTACCGTTCGCGAGCCGATATTTGTTGACGAGCTTCACGACCCCTGTTCTTGTCT 111
DB 32 AAGAGTTCGCGAGCCGATATTTGTTGACGAGCTTCACGACCCCTGTTCTTGTCT 111
QY 112 CCAAGGGAAGAGCCACCTCTCCGACGAGCCACGACAGTGT----- 156
DB 52 ValGlyAspArgValThrIleThrCysLysSerSerGlnSerValLeuTyrSerSerAen 71
QY 157 ACTAGACGACTTACCTGAGCTGTGACGAGCAAGAACTGGCGGAGCTCCGAGCTCTCCTC 216
DB 72 GlnLysAsnTyrLeuAlaThrPyrGlnGlnLysProGlyValAlaProLysLeuLeuIle 91
QY 217 TATGTGATCCACGAGGCGACCTGTCATGACGAGCAAGAGTTCAGTGGAGTCCGCGG 276
DB 92 TyrTPAlaSerThrArgLysSerGlyValProSerArgPheSerGlySerGlySerGly 111
QY 277 AAGAGCTTACTCTCACTCCATCAGTACGAGCTGAGAGCTGGAAGATTGTCAGTGTACTGT 336
DB 112 ThrAspPheThrPheThrIleSerSerLeuGlnProGlyAspIleAlaThrTyrCys 131
QY 337 CAGCAGTATGATGATGCTCAGCTCAGACCTCAGATCACTTGGGCGAGGAGCAAGG 396
DB 132 HAsGlnTyrLeuSerSer-----TyrPheGlyGlnGlyThrLysVal 146
QY 397 GAGATCAACGAACTGTGCTGACCATCTGTCTGCGCGGCTGCGAGGTGCT 456
DB 147 GlnIleLysSer-----SerGlyGlyGlySerGlyGly 159
QY 457 GAGTACAGTGGAGAGTGGCTCCAGAGTGGAGCTGGTGGAGTGGAGAGGCTGCTCCAG 516
DB 160 GlySerGlyGlyGlySerGlyValAlaGlnLeuValAlaGlnSerGlyGlyValAlaGln 179
QY 517 CCTGGAGAGTCCCTGAGACTCTCTGTGACGCTCGATTCCTCCCTCGAAGAGCTTGTGT 576
DB 180 ProGlyLysSerLeuArgLeuArgLeuSerCysSerSerSerGlyPheIlePheSerAspAsnTyr 199
QY 577 ATGCACTGGGTCGCGCAGGCTCTAGGCAAGGAGCTGAGTGGAGTGGAGTTCATATCAT 636
DB 200 MetTyrTPValAlaArgLysAlaProGlyLysGlyLeuGlnTyrValAlaThrIleSerAsp 219
QY 637 GATGGAAGACATAAATACGACAGACTCCGTCGAAGGCGCATTCACCTCTCCAGAGAC 696
DB 220 GlyGlySerTyrThrTyrTyrProAspSerValLysGlyArgPheThrIleSerArgAsp 239
QY 697 ACTTCAAGAAACAGCGGTATATTAATAATGACAGAGCTGAGAACTGAGAGCAGCGCTGTC 756
DB 240 AsnSerLysAsnThrIleuPheLeuGlnMetAspSerLeuArgProGlnAspThrGlyVal 259
```

```

QY 757 TATTACTGTGCGAGAGATCAGAGAGCTGTTGGTACTATGACCACTACTACGTTTGAC 816
DB 260 TyrPheCysAlaArg-----GlyTyrTyrArgTyrGlnGlyAlaMetAsp 274
QY 817 GTCTGGGCAAGAGGACCGAGCTCCGCTCCCTCTCAGAG-----TCCGAACA 864
DB 275 TyrTPGlyGlnGlyThrProValThrValSerSerProArgLeuGlnValAspGln 294
QY 865 AAAGTATCAGCGAAGAAAGATCTGAAC 891
DB 295 LysLeuIleSerGlnGlnAspLeuAsn 303

RESULT 6
US-10-634-862-11
/ Sequence 11, Application US/10634862
/ Publication No. US20040048383A1
/ GENERAL INFORMATION:
/ APPLICANT: RUDERT, FRITZ
/ APPLICANT: GE, LIMING
/ APPLICANT: ILAG, VIC
/ TITLE OF INVENTION: NOVEL METHOD AND PHASE FOR THE IDENTIFICATION OF
/ TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIC
/ TITLE OF INVENTION: (POLY) PEPTIDE COMPLEX
/ FILE REFERENCE: MORPHO/9
/ CURRENT APPLICATION NUMBER: US/10/634,862
/ CURRENT FILING DATE: 2003-08-06
/ PRIOR APPLICATION NUMBER: US/09/495,880A
/ PRIOR FILING DATE: 2000-02-01
/ PRIOR APPLICATION NUMBER: PCT/EP98/04836
/ PRIOR FILING DATE: 1998-08-03
/ PRIOR APPLICATION NUMBER: EP 97 11 3319.4
/ PRIOR FILING DATE: 1997-08-01
/ NUMBER OF SEQ ID NOS: 50
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 11
/ LENGTH: 456
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: ompA-FLAG-acFv (anti-
US-10-634-862-11

Alignment Scores:
Pred. No.: 1.55e-57 Length: 456
Score: 926.50 Matches: 190
Percent Similarity: 75.428 Conservative: 37
Best Local Similarity: 63.128 Mismatches: 49
Query Match: 54.098 Indels: 25
DB: 15 Gaps: 6

US-09-194-164-13 (1-918) x US-10-634-862-11 (1-456)
QY 7 ATGAAAAAACCCTATGCGGATGCGAGTTCAGTGGCTGTTTGGCTACCGTTGGCAG 66
DB 1 MetLysLysThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrValAlaGln 20
QY 67 GCC-----GATATGTGTGACGAGTCTCCAGGACCCCTGCTTGTCTCCAGG 117
DB 21 AlaAspTyrLysAspIleValAlaMetThrGlnSerProSerSerLeuThrValThrAlaGly 40
QY 118 GAAAGAGCACCCTCTCCGACGAGGCGACGTCAGACTGTTAGTACGAGC----- 165
DB 41 GlnLysValThrMetSerCysThrSerSerGlnSerLeuPheAsnSerGlyLysGlnLys 60
QY 166 ---TACTTAAGCTGTGATCAGAGCAAACTGGCCAGGCTCCAGGCTCTCATTCATGTGT 222
DB 61 AsnTyrLeuThrThrTyrGlnGlnLysProGlyGlnProGlyValLeuLeuIleTyrTP 80
QY 223 GCATCAGCAGGCGCAGCTGCGATGCGACAGTTCAGTGGAGTGGAGTCCGCGAGCAGAC 282
DB 81 AlaSerThrArgLysSerGlyValProAspArgPheThrIleGlySerGlySerGlyThrAsp 100
```

```
QY 283 TTCACTCTCAACATCACTGAGACCTGGAAGATTTCGATGATTAATCTGTCAGCAG 342
    |||||
    :
Db 101 PheThrIleuThrIleSerValGlnAlaGluAspLeuAlaValTyrCysGlnAsn 120
    |||||
    :
QY 343 TATGTATGCTCAGCTCAGACACCTCAGATCTTGGCGGAGGAGACAGGTGGAGATC 402
    |||||
    :
Db 121 AspTyrSerAsnPro-----LeuThrPheGlyGlyGlyThrValGluGluLeu 136
    |||||
    :
QY 403 AAACGAATGTGGCTGACCATCT-----GTCTCTGGCGGT 438
    |||||
    :
Db 137 LysArgAlaGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly 156
    |||||
    :
QY 439 GGGGCTTCGGAGGTGTGATCAGGTGAGGCTCCAGGTGACGTGTGGAGTCT 498
    |||||
    :
Db 157 GlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly 176
    |||||
    :
QY 499 GGGGAGGCGTGGTCCAGGCTGGGAGGCTCCGTAAGACTCTCTGTGACGCTCTGATTC 558
    |||||
    :
Db 177 GlyGlyAspLeuValLysProGlyGlySerLeuLysSerCysAlaAlaSerGlyPhe 196
    |||||
    :
QY 559 CCTTCGAAGCTTTGCTATGACCTGGTCCGCGACGCTCTAGGCAAGGGCTGAGTGG 618
    |||||
    :
Db 197 SerPheSerSerTyrGlyMetSerTyrValArgGlnThrProAspLysArgLeuGluTyr 216
    |||||
    :
QY 619 GTGGCAGTTATATCATATGATGAGAGCACTAAATACAGACACTCCGTAAGGGCCGA 678
    |||||
    :
Db 217 ValAlaThrIleSerAsnGlyGlyGlyTyrThrTyrTyrProAspSerValLysGlyArg 236
    |||||
    :
QY 679 TTCACCATCTCCAGAGACACTTCCAGAGACAGCGGTGATCTAAATAAGAACAGCTGAGA 738
    |||||
    :
Db 237 PheThrIleSerThrArgAspAsnAlaLysAsnThrLeuGlnMetSerSerLeuLys 256
    |||||
    :
QY 739 ACTGAGAGACGCGCTGTCTATTACTGTGCGAGAGATCAGAGCTGTGGTGAATATGAC 798
    |||||
    :
Db 257 SerGluAspSerAlaMetTyrTyrCysAlaArgArgGluArg-----TyrAsp 272
    |||||
    :
QY 799 CACTACTACGCTTGGACGCTCTGGGGAAGGAGACACGCTCACGCTCTCTAGAGATCC 858
    |||||
    :
Db 273 Glu---AsnGlyPheAlaTyrTyrGlyGlnGlyThrLeuValThrValSerAlaSerGly 291
    |||||
    :
QY 859 GAA 861
    |||||
    :
Db 292 Glu 292
    |||||
    :
RESULT 7
US-09-983-580-6
; Sequence 6, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
; APPLICANT: Filipula, David R.
; APPLICANT: Wang, Maoliang
; TITLE OF INVENTION: No. US20020151061A1 Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983,580
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Kabat
; NAME/KEY: UNSURE
; LOCATION: (232)
; OTHER INFORMATION: May be any amino acid.
```

```
; NAME/KEY: UNSURE
; LOCATION: (234)
; OTHER INFORMATION: May be any amino acid.
; NAME/KEY: UNSURE
; LOCATION: (239)
; OTHER INFORMATION: May be any amino acid.
US-09-983-580-6

Alignment Scores:
Pred. No.: 4.27e-55 Length: 283
Score: 892.00 Matches: 181
Percent Similarity: 76.92% Conservative: 29
Best Local Similarity: 66.30% Mismatches: 47
Query Match: 52.07% Indels: 16
DB: 9 Gaps: 5

US-09-194-164-13 (1-918) x US-09-983-580-6 (1-283)

QY 70 GATATTGTGTGACGACGATCTCCAGACACCTGCTTTGTCTCCAGGGGAAAGACCCACC 129
    |||||
    :
Db 1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20
    |||||
    :
QY 130 CTCTCTCAGAGGCGCAGTCAAGTGT-----AGTACAGACTACTTACCTGTATCCAG 183
    |||||
    :
Db 21 IleThrCysArgAlaSerGlnSerLeuValSerIleSerAsnTyrLeuAlaTyrPyrGln 40
    |||||
    :
QY 184 CAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGATGATTCATCCAGGCGCACCTGGC 243
    |||||
    :
Db 41 GlnLysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGluSerGly 60
    |||||
    :
QY 244 ATGCCAGACAGGTTGAGGAGGAGGCTCCGGAAGACCTTCACTCAGTCACTCAGTGA 303
    |||||
    :
Db 61 ValProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSer 80
    |||||
    :
QY 304 CTGAGCCTGAAGATTGTGACGTGATTAATCTGTCAGCAGTATGATGAGCTCACTCAGACA 363
    |||||
    :
Db 81 LeuGlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSer-----Leu 97
    |||||
    :
QY 364 CCTCAGATCATCTTTGGCGGAGGAGGACCAAGGTGAGATCAACGAACTGTGGCTGACCA 423
    |||||
    :
Db 98 ProGluTyrPheThrPheGlyGlnGlyThrLysValGluIleLysGlySer----- 113
    |||||
    :
QY 424 TCTGTCTCGGCGGCGGAGGCTCCGAGGTGATCAGGTGAGGAGTGGCTCCAGGTTG 483
    |||||
    :
Db 114 -----ThrSerGlySerGlyLysProGlySerGlyGlnGlySerThrLysGlyGlnVal 131
    |||||
    :
QY 484 CAGCTGTGAGATCTGGGAGGAGCGTGTCCAGCTCGGAGATCCCTGAGACTCTCTGT 543
    |||||
    :
Db 132 GlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuAspLeuSerCys 151
    |||||
    :
QY 544 GAGCCTCTGATTCCTTTCAGAAAGCTTTGCTATGACCTGGTCCGCGCAGGCTCTAGGC 603
    |||||
    :
Db 152 AlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTyrValArgGlnAlaProGly 171
    |||||
    :
QY 604 AAGGGCTGAGAGTGGGTGAGTATATCA-----TATGATGAAAGACTAAATATCTAC 657
    |||||
    :
Db 172 LysGlyLeuGluTyrPheValSerValIleSerGlySerThrAspGlyGlySerThrTyr 191
    |||||
    :
QY 658 GCAGACTCCGTGAAGGCGCATTCACATCTCCAGAGACACTTCCAGAGACAGGTGAT 717
    |||||
    :
Db 192 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 211
    |||||
    :
QY 718 CTAAAAATGAACAGCTGAGAACCTGAGACACGCGTGTCTTACTGTGCGAGAGATCAG 777
    |||||
    :
Db 212 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArgGlyArg 231
    |||||
    :
QY 778 -----AGCTGTGGTGAATGACCACTATGACAGTCTGAGGCGCAAA 828
    |||||
    :
Db 232 ***Gly***SerLeuSerGly***TyrTyrTyrTyrHisTyrPheAspTyrTrpGln 251
    |||||
    :
QY 829 GGGACCAAGGTCCAGCTCTCTCAGAGATCCGAAACAAA 867
    |||||
    :
Db 252 GlyThrLeuValThrValSerSerLysLysLysLys 264
    |||||
    :
```



## RESULT 8

US-09-985-442-6  
Sequence 6, Application US/09985442  
Patent No. US20020156248A1  
GENERAL INFORMATION:  
APPLICANT: Filipula, David R.  
APPLICANT: Filipula, David R.  
APPLICANT: Whitley, Marc D.  
TITLE OF INVENTION: NO. US20020156248A1 Method for Targeted Delivery of Nucleic Acid  
FILE REFERENCE: 0977.2300003  
CURRENT APPLICATION NUMBER: US/09/985,442  
PRIOR FILING DATE: 2001-11-02  
PRIOR APPLICATION NUMBER: 09/420,592  
PRIOR FILING DATE: 1999-10-13  
PRIOR APPLICATION NUMBER: 60/104,949  
PRIOR FILING DATE: 1998-10-20  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 283  
TYPE: PR  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Kabat  
NAME/KEY: UNSURE  
LOCATION: (232)  
OTHER INFORMATION: May be any amino acid.  
NAME/KEY: UNSURE  
LOCATION: (234)  
OTHER INFORMATION: May be any amino acid.  
NAME/KEY: UNSURE  
LOCATION: (239)  
OTHER INFORMATION: May be any amino acid.  
US-09-985-442-6

## Alignment Scores:

Pred. No.:	4,27e-55	Length:	283
Score:	892.00	Matches:	181
Percent Similarity:	76.92%	Conservative:	29
Best Local Similarity:	66.30%	Mismatches:	47
Query Match:	52.07%	Indels:	16
DB:	9	Gaps:	5

US-09-194-164-13 (1-918) x US-09-985-442-6 (1-283)

QY 70 GATATTGTGTGACGAGTCTCCAGGACCCGTTGTCTCCAGGGGAAGAGCCACC 129  
DB 1 AepilegImetThrlGlnSerProSerSerLeuSerAlaSerValGlyAapArgValThr 20  
QY 130 CTCTCTGAGGAGGAGTCTCCAGGAGTGT-----AGTACAGCTACTTACCTGATACAG 183  
DB 21 IletHrCyArgAlaSerSerLeuValSerIleSerAsnTyrIleuAlaTrpTyrGln 40  
QY 184 CAGAAACTGGCCAGGCTCCAGGCTCTCATCTATGTGTCATCCACCGGCCACTGSC 243  
DB 41 GlnLysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGly 60  
QY 244 ATGCAGACAGGTTGAGTGGGAGTGGGTCGGGACAGACTTCACTCCATCCATCAGTAGA 303  
DB 61 ValProSerArgPheSerSerIleSerGlySerGlyThrAapPheThrLeuThrIleSerSer 80  
QY 304 CTGAGACCTGAAAGATTTTGCAGTGTATTACTGTACAGAGTATGTAGTCACTCAGACA 363  
DB 81 LeuGlnProGlnAapPheAlaThrTyrTyrGlyGlnGlnTyrAaSer-----Leu 97  
QY 364 CTTGATCATCTTTGGCGGAGGAGGACCAAGGTGAGATCAAAAGAACTGTGCTGCACCA 423  
DB 98 ProGlnTrpThrPheGlyGlnGlyThrLysValGlnIleTyrGlySer----- 113  
QY 424 TCTGTCTGGCGGTGGCGGCTTCGGAGGAGTGTGATCAGTGTGAGAGGTGCTCCAGGTG 483

DB 114 -----ThrSerGlySerGlyLysProGlySerGlyGlnGlySerThrLysGlyVal 131  
QY 484 CAGCTGTGAGTCTGGGAGGAGCGGTGTCCAGGCTGGAGGTCCTGAGACTCTCTGT 543  
DB 132 GlnLeuValGlnSerGlyLysGlyLeuValGlnProGlyGlySerLeuArgLeuSerCys 151  
QY 544 GAGAGCTCTGAGTTCCTCCAGAACTTGTCTATGACATGGGTCCGACGCTCAGGC 603  
DB 152 AlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTyrValArgGlnAapProGly 171  
QY 604 AAGGAGCTGAGTGGGTGAGTGTATATCA-----TATGATGAGACACTAAATCACTAC 657  
DB 172 LysGlyLeuGlnTrpValSerValIleSerGlyLysThrAapGlySerThrTyr 191  
QY 658 GCAGACTCCGTGAAGGCGGATTCACCATCTCCAGAGACATTCACAAAGACGTGTAT 717  
DB 192 AlaAapSerValLysGlyArgPheThrIleSerArgAapAaSerLysAaThrLeuTyr 211  
QY 718 CTMAAATGACAGCTGAGACTGAGACACAGGCTGTCTATTACTGTGCGAGATCAG 777  
DB 212 LeuGlnMetCAsnSerLeuArgAlaGlnAapThrAlaValTyrTyrCysAlaArgGlyArg 231  
QY 778 -----AGCTGTGGGTGACTATGACACTACTACAGTGTGAGCGTGGGAGCA 828  
DB 232 \*\*\*Gly\*\*\*SerLeuSerGly\*\*\*TyrTyrTyrTyrTyrTyrTyrTyrTyrTyr 251  
QY 828 GGAACACGCTCAGCGTCTCTCCAGAGATCCGACAAAAA 867  
DB 252 GlyThrLeuValThrValSerSerLysLysLysLys 264

## RESULT 9

US-09-956-086-3  
Sequence 3, Application US/09956086  
Patent No. US2002015498A1  
GENERAL INFORMATION:  
APPLICANT: FILIPULA, DAVID  
APPLICANT: SHORR, ROBERT  
APPLICANT: WHITLOW, MARC  
LEE, LIHSYNG S.  
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,086  
FILING DATE: 20-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,821  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH U.  
REGISTRATION NUMBER: 40,679  
REFERENCE/DOCKET NUMBER: 0977.2280003  
TELECOMMUNICATION INFORMATION:

```

;
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-956-086-3

Alignment Scores:
Pred. No.: 9.63e-55 Length: 263
Score: 887.00 Matches: 180
Percent Similarity: 77.24% Conservative: 27
Best Local Similarity: 67.16% Mismatches: 45
Query Match: 51.78% Indels: 16
DB: 9 Gaps: 5

US-09-194-164-13 (1-918) x US-09-956-086-3 (1-263)
QY 70 GATATTGTGTGACGAGCTCCAGGACCCGTGTTGTCTCCAGGGGAAAGGCCACC 129
Db ||||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
QY 130 CTCTCCCTGCGAGGCGCAGTCAAGAGT---AGTACGACCTACTTAAAGCTGTACCG 183
Db ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
21 ILethrCyArAlaSerGlnSerLeuValSerIleSerAsnTyrlleuAlaTrpGln 40
QY 184 CAGAAACCTGGCAGGCTCCAGGCTCCATCATGTATGTCATCCACGAGGCGCAGTGGC 243
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
41 GlnIleProGlyAlaProIleuValSerIleValAlaSerSerLeuGlnSerGly 60
QY 244 ATGCCAGACAGGTTCAAGTGGAGTGGTCCGGACAGACTTCACTCCATCAGTAA 303
Db ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 ValProSerArgPheSerGlySerGlyThrAspPheThrIleuThrIleSerSer 80
QY 304 CTGAGACCTGAAGATTGTGAGTGATATCTGACAGAGTATGTATGCTCAGCTCAGACA 363
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
81 LeuGlnProGlnAspPheAlaThrTyrcysGlnGlnIleAsnSer-----Leu 97
QY 364 CCTCAATCATCTTCCGCGGAGGACCAAGGTGAGATCAAGTGGAGTGGCTCCAGTGA 423
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
98 ProGlnThrPheThrGlyGlnGlyThrIleValGlnIleGlySer----- 113
QY 424 TCTGTCTCTGGCGGTGGCGGTTCCGAGGTGATCAAGTGGAGTGGCTCCAGTGA 483
Db ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
114 -----ThrSerGlySerGlyLysProGlySerGlyGlnGlySerThrIleVal 131
QY 484 CAGCTGTGAGTCTTGGGAGGCGGTGTCAGCTCCGAGGCTCCAGTCTCTCTGT 543
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
132 GlnLeuValGlnSerGlyGlyLeuValGlnProGlyIleSerLeuArgLeuSerCys 151
QY 544 GCAGCCTTGATTTCCCTCAGAGCTTATGATCATCTGATCCGCGGAGGCTTAAGCC 603
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
152 AlaAlaSerGlyPheThrPheSerSerTyrlaMetSerTrpValArgGlnAlaProGly 171
QY 604 AAGGGGCTGAGTGGTGGCAGTTATATCA-----TATGATGAAGACATAATATCA 657
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
172 LysGlyLeuGlnIleValSerValIleSerGlyLysThrAspArgIleThrIleTy 191
QY 658 GCAGACTCCGTTGAAGGCGGATTCACCATCTCCAGACACTTCCAGAAACGAGTAT 717
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
192 AlaAspSerValLysIleArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 211
QY 718 CTAAATGAACAGCTGAGAACTGAGACACGCGTGTATATTACTGTCCGAGATCG 777
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
212 LeuGlnMetAsnSerLeuArgIleAspThrIleValIleTyrcysAlaArgGlyAs 231
QY 778 -----AGCTGTGGGTGACTATGACACCTACTACGAGTGTGAGCGGCAAA 828
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
232 ***Gly***SerIleuSerGly***TyrlTyrlTyrlTyrlIleTyrlPheAspTyrlTrpGln 251
```

```

QY 829 GGAGCCAGCGTCACCGTCTCTCA 852
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
252 GlyThrLeuValThrValSerSer 259

RESULT 10
US-09-956-087-3
; Sequence 3, Application US/09956087
; Patent No. US20020161201A1
; GENERAL INFORMATION:
; APPLICANT: FILIPULA, DAVID
; MANG, MAOLIANG
; SHORR, ROBERT
; WHITLOW, MARC
; LEE, LHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1102 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,087
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: not relevant
TOPOLOGY: not relevant
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-956-087-3

Alignment Scores:
Pred. No.: 9.63e-55 Length: 263
Score: 887.00 Matches: 180
Percent Similarity: 77.24% Conservative: 27
Best Local Similarity: 67.16% Mismatches: 45
Query Match: 51.78% Indels: 16
DB: 9 Gaps: 5

US-09-194-164-13 (1-918) x US-09-956-087-3 (1-263)
QY 70 GATATTGTGTGACGAGCTCCAGGACCCGTGTTGTCTCCAGGGGAAAGGCCACC 129
Db ||||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
```

```

QY 130 CTCTCTGAGGGCCAGTCAAGTGT-----AGTACGACTTACTTACCTGTACCG 183
DB 21 ILEMTCYARXALASERGLSERLEUVALSERLIESERATRYLEUVALTRYRGLN 40
QY 184 CAGAAACCTGGCCAGGCTCCAGGCTCCATCTATGTGACATCCAGGCGCACTGGC 243
DB 41 GINLYSPROGILYLYALALPROLYLEULEULIETRYALALASERLEUVALSERGLY 60
QY 244 ATCCAGACAGGTTCACTGAGCAGTGGCTCCGAGACAGACTTCACTTCCATCAGTACA 303
DB 61 VALPROSERARGPHESEGLYSEGLYSEGLYTHNAPHETHRLEUTHRILLESER 80
QY 304 CTGGAGCCCTGAGATTTTGCAGTATTACTGTACAGTATGAGTACCTCAGTACACA 363
DB 81 LEUGINPPOGILUAPPHALATHRYTRYCYGGLNGINTRYANSE-----LEU 97
QY 364 CCTCATCATCTTGGCCGAGGACCAAGTGGAGATCAAGAACTGTGGCTGACCA 423
DB 98 PROGILUTPRTHRPHGLYGLNGLYTHRYVALGLULIELYGLYSE----- 113
QY 424 TCTGTCTGCGGCTGGCGGTTCCGAGGTGGTGAATCAGTGGAGGTGCTCCAGTG 483
DB 114 -----THNserGLYserGLYSPROGLYserGLYGLULYserTHRlyseGLYVAL 131
QY 484 CAGCTGTGGAGTCTGGGGGAGCGGTGTCAGCTGGGAGGTCCCTGAGACTTCTCTGT 543
DB 132 GINLEUVALIGLUSERGLYGLYGLYLEUVALGINPROGLYGLYSELEUARGLEUSERY 151
QY 544 GCAGCCTGTGATTCCTCCCTTCAGAGCTTGTATGACTGGGTCCGAGGCTCGAAGC 603
DB 152 ALAALASERGLYRPHETHRPHESERETRYALAMESETTRPVALARGINLAPROGLY 171
QY 604 AAGGGCTGAGTGGGTGGCTGACTTATATCA-----TATGATGAAGCACTAATATAC 657
DB 172 LYSEGLYLEUGILUTPRVALSERVALILLESERGLYLYSTHNASPGLYGLYSETHRlyTRY 191
QY 658 GCAGTCTCCGTGAAGGCGGATTCACATCTCCAGAGACACTTCCAGAAACCGGTGAT 717
DB 192 ALAASERVALYLYGLYARPHETHRILLESERARGAPASERLYSANTHRILEU 211
QY 718 CTAAATGAACAGCCTGAGAACTGAGACAGCGGTCTATTACTGTGGCAGATGAG 777
DB 212 LEUGINMEASERLEUARGALAGLUPRTHRALVALTRYTRYCYALARGGLYARG 231
QY 778 -----AGCTGTGGGTGACTATGACCACTACCTAGGTTTGGAGCTGGGCAAA 828
DB 232 ***GLY***SERLEUserGLY***TYRTRYTRYTRYTRYTRYRPHASPRYTRPGLYGIN 251
QY 829 GGGACCAAGGTCAAGCTCTCTCA 852
DB 252 GLYTHRLEUVALTHRVALSER 259

RESULT 11
US-10-422-628-48
; Sequence 48, Application US/10422628
; Publication No. US20040014174A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: MAYFIELD, Stephen P.
; APPLICANT: FRANKLIN, Scott E.
; TITLE OF INVENTION: EXPRESSION OF POLYPEPTIDES IN CHLOROPLASTS, AND COMPOSITIONS AND
; FILE REFERENCE: FOR EXPRESSING SAME
; CURRENT APPLICATION NUMBER: US/10/422,628
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/375,129
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/434,957
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48

```

```

; LENGTH: 630
; TYPE: PR
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single-chain antibody
US-10-422-628-48

Alignment Scores:
Pred. No.: 2,856-53 Length: 630
Score: 866.50 Matches: 180
Percent Similarity: 76.12% Conservative: 24
Best Local Similarity: 67.16% Mismatches: 51
Query Match: 50.58% Indels: 13
DB: 15 Gaps: 4

US-09-194-164-13 (1-918) x US-10-422-628-48 (1-630)
QY 58 GTTGGCAG-----GCCGATATTGTGTGACGAGTCTCCAGGACCCGTGCTTGTCTCA 114
DB 2 VALAAGINALALASERSERGLULEUTHRGINSERPROGLYTHRLEU SERLEU 21
QY 115 GGGGAAAGACCCACTCTCTGACAGGCGACGTCAAGTGTATGACAGTACTTACGC 174
DB 22 GLYLUARGALATHRLEU SERCYARGALASERGLINSERVALSERVALTRYLEU 41
QY 175 TGTACCCAGCAGAACTGGCCAGGCTCCAGGCTCTCATATTATGTGATCCAGCAG 234
DB 42 TRYTRYGLINGILYSPROGLYGLINLAPROGLYLEULEULIETRYGLYALASER 61
QY 235 GCCACTGGCATGCCAGACAGGTTCACTGAGTGGGTCCGAGGACAGACTTCACTCA 294
DB 62 ALATHRGILYILEPROASPRGPHESERGLYSEGLYTRYTHNASPHETHR 81
QY 295 ATCACTAGACTGAGACCTGAAGATTTCAGTGTATTACTGTACAGATGTAGTCA 354
DB 82 ILESERARGLEUGILUPROGLUAPPHALALVALTRYTRYCYGGLNGINTRYGLY 101
QY 335 CCTCAGACACTCAGATCACTTTCGGCGGAGGACCAAGTGGAGATCAAACTGTG 414
DB 102 PRO-----THRPHGLYGLYGLYTRYLYSVALGLULIELYASRGT 115
QY 415 GCTGCACATCTGTCTGTGGCGGTGGCGGTTCCGAGGAGGTGATCAGTGGAGTGGC 474
DB 116 -----SERSERGLYGLYGLYGLYGLYGLYGLY-----GLYGLYGLY 129
QY 475 TCCAGTGAAGTGTGGTGGAGTCTGGGAGGCGGTGTCAGCTGGAGGTCCCTGAGA 534
DB 130 SERARGSERLEUGLUGLNSERGLYALAGLUVALLYLYSPROGLYSESERVALY 149
QY 535 CTCTCTGTGACCTCTGAGATTCCTTCAGAGACTTGTCTATGACACTGGTCCGCA 594
DB 150 VALSERCYLYSALASERGLYGLYSEPHESERTRYALALIASANTPRVALRG 169
QY 595 GCTTAGGCAAGGGGCTGAGTGGGTGACGTTATATCATATGATGAAGCACTAATAC 654
DB 170 ALAAGLNGLYGLNGLYLEUGILUTPRMETGLYGLYLEUMETPROILEPHGLYTHR 189
QY 655 TACGAGACTCCGTGAGAGGCGGATTCACATCTCCAGACACTTCCAGAAACCGGTG 714
DB 190 TYRILAGLNLSPHNEGLUAPRGLYTHRILETHRALAAPVALSERTHRTHR 209
QY 715 TATCTAAATGAACAGCCTGAGAACTGAGACAGCGCTGTCTATTACTGTGCGAGAT 774
DB 210 TYRMECTGLNLEU SERGLYLEU THRTRYGLIUNAPRTHRALAME TRYTRYCY 229
QY 775 CAGAGCCGTGGGTGATGATGACACACTACAGGTTTGGAGTGGGCAAGGAGCC 834
DB 230 ALATYRMECTLEUGILUPRTHVALTHRALAGLGLYLEUAPVALTRPGLYLYSE 249
QY 835 ACGGTCAAGCTCTCTCAGATCC 858
DB 250 THRVALTHRVALSERPROALASER 257

```



US-09-194-164-13 (1-918) x US-10-409-938-21 (1-279)

Qy 67 GCGCATATTCGCTTTACGACGCTCCAGGACCCCTCTTTTCTCTCCAGGGGAAAGACC 126

Db 21 AaaapillevallennhrincinsierProGlytrnhrLeuSerLeuSerIaaGlyGluAAGlaa 40

```

QY      127  ACCCTCTCTGTGAGGGCCAGCTGAGAGTGTTAGTAGAGCTACTTACCTGTGATCCAGAG 166
Db      41  ThrLeuSerCySArAlaSerAlaSerValSerSerGlySerLeuAlaTrpYrGlnGln 60
QY      187  AAACCTGGCCAGGCTGCCAGGCTCTCTCATCTATGTGTGATCCACAGGGCCACTGGCATG 246
Db      61  LysPProGlyGlnAlaPProArgLeuLeuIleTrpGlyAlaSerThrArgAlaThrGlyIle 80
QY      247  CCAGACAGGTTCAAGTGGCCAGTGGGTTCCGGGACAGACTTCACTCTCAACCATCAGTAGACTG 306
Db      81  ProAlaPArgPheSerGlySerIlySerGlyYrThrAspPheThrLeuThrIleGlyArgLeu 100
QY      307  GAGCGTGAAGATTGTTGACGTATTAATCACTGTCAGCAGATGATGATGATCACTCAGACACCT 366
Db      101  GluPProGluAspLeuAlaValAlaYrTrpCySglnGlnTrpGlyYrThrSerPro----- 117
QY      367  CAGATCACTTTCGCGCGAGGAGGACCAAGGTGAGATCAACAGAACTGTGGCTGCACCATCT 426
Db      118  ---YrThrPheGlyGlnGlyYrThrYrSValAspIleYrArg----- 130
QY      427  GTCTGTGGCGGTGGCGGTTCCGAGAGGTGTGATCAAGGTGAGAGTGGC-----TCC 477
Db      131  -----GlyGlyGlyGlySerIlyGlyGlyGlySerGlyGlyGlySerArgSer 148
QY      478  CAGGTGACGCTGTGTGAGTCTGTGGGGGAGCGCGTGTCCACCTGGGAGGTCCTCGAGACTC 537
Db      149  GlnValGlnLeuValGlnSerIlyAlaGluValIlyLysPProGlySerSerValGlnVal 168
QY      538  TCCTGTGACGCTCTGTGATTCCTCCCTTCAGAACTTGTGATGACACTGTGGGTCCGCCAGGCT 597
Db      169  SerGlySValAspSerGlyGlyYrThrPheSerMetYrGlyYrPheAsnTrpValArgGlnAla 188
QY      598  CTAGGCAAGGGCGCTGAGTGGGTGGCGACGTTATATCATATGATGAAGACCTAAATACTAC 657
Db      189  ProGlyHleGlyLeuGlyLutPMetGlyGlyIleIleProIlePheGlyYrThrSerAsnYr 208
QY      658  GCAGACTCCGTGAGAGGCGCGATTCACATCTCCAGAGACACTCCCAAGAACCGGTGTAT 717
Db      209  AlaGlnLysPheArgGlyArgValIyrPheThrAlaAspGlnAlaThrSerThrAlaYr 228
QY      718  CTAAATAATGACACGCTGAGACTGAGACAGCAGCGCTGTATTATCTGTGTGAGAGATCAG 777
Db      229  MetGluLeuThrAsnLeuArgSerSerAspPheThrAlaValAlaYrTrpYrSValArgAsp--- 247
QY      778  AGCCTGTGGT-----GACTATGACCACTACTACGCT----- 810
Db      248  -----PheGlyProAspTrpGluAspGlyLysAspSerYrAspGlySerGlyArgGlyPhe 265
QY      811  TTGACGCTCTGGGGGCAAGAGGACCAACGCTGACCCGTCTCTCA 852
Db      266  PheAspPheTrpGlyGlnGlyYrThrLeuValThrValSerSer 279

RESULT 15
US-10-423-847-10
; Sequence 10, Application US/10423847
; Publication No. US20040009166a1
; GENERAL INFORMATION:
; APPLICANT: FILIPULA, DAVID RAY
; APPLICANT: YANG, KAREN
; APPLICANT: BASU, AMARTYA
; APPLICANT: WANG, MAOJIANG
; TITLE OF INVENTION: SINGLE CHAIN ANTIGEN-BINDING POLYPEPTIDES FOR POLYMER
; FILE REFERENCE: 213.1180
; CURRENT APPLICATION NUMBER: US/10/423,847
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 09/791,578
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/791,540
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/069,842
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/044,449

```

```
/ PRIOR FILING DATE: 1997-04-30
/ PRIOR APPLICATION NUMBER: 60/050,472
/ PRIOR FILING DATE: 1997-06-23
/ PRIOR APPLICATION NUMBER: 60/063,074
/ PRIOR FILING DATE: 1997-10-27
/ PRIOR APPLICATION NUMBER: 60/067,341
/ PRIOR FILING DATE: 1997-12-02
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 10
/ LENGTH: 252
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic 2-7-8C-1
/ US-10-423-847-10

Alignment Scores:
Pred. No.: 4 42e-52 length: 252
Score: 849.50 Matches: 170
Percent Similarity: 72.04% Conservative: 31
Best Local Similarity: 60.93% Mismatches: 51
Query Match: 49.59% Indels: 27
DB: 15 Gaps: 5

US-09-194-164-13 (1-918) x US-10-423-847-10 (1-252)

QY 70 GATATTGTGTGACGCGAGTCTCCAGGACCCCTGTTGTCGAGGGGAAAGACCACC 129
    |||||  ::::|  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 Aspl1g1m1merThrglnSerProserSerleuSerAlaSerValGlyAspArgValThr 20

QY 130 CTCTCCTGAGGGCCGCGAGTGTAGAGAGTACTTACCTGTTACCGAGAGAA 189
    ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|
Db 21 l1ethrCysArgAlaSerGlnGlnIle---ArgAsnTyrleuAlaTrrPtyrGlnGlnLys 39

QY 190 CCTGGCCAGGCTCCAGGCTCTCATCTATGTCATGCCACCGAGGCCACTGGCATGCCA 249
    |||||  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|
Db 40 ProGlyIyAlaProIySleuLeuIleTyrAlaAlaSerThrleuGlnSerGlyValPro 59

QY 250 GACAGGTTGAGTGGAGTGGGTCGGGAGACAGACTTCATCTCCATCAGTAGACTGAG 309
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 60 SerArgPheSerGlySerGlySerGlyThrAspPheThrleuThrIleSerSerleuGln 79

QY 310 CCTGAAGATTTCAGTGTATTACTGTCCAGCAGTATGTAAGTCACTCAGACCTCAG 369
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 80 ProGluAspValAlaThrTyrCysGlnArgTyrAsnArgAlaPro----- 95

QY 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAAGCACTGGGCTGCACCATCTGTC 429
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 96 TyrThrPheGlyGlnGlyThrIySValGlnIleLysGlySer----- 109

QY 430 TCTGGCGGTGGCGGTTCCGAGGTGGATGATCAGTGAAGTGGCTCCAGGTGACGCTG 489
    ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|
Db 110 ThrSerGlySerGlySproGlySerGlyGlnGlySerThrIySValGlnValGlnLeu 129

QY 490 GTGGAGTCTGGGGGAGCGGTGCTCCAGCTGGGAGGTCCTTGAGATCTTCTGTGAGCC 549
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 130 ValGlnSerGlyGlyGlyLeuValGlnProGlyArgSerleuArgLeuSerCysAlaIle 149

QY 550 TCTGATTCCTCCCTTCAGAGCTTTGCTATGACCTGGGTCGGCCAGGCTTAAGGCAAGGG 609
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 150 SerGlyPheThrPheAspAspTyrAlaMetHisIleTrrValArgGlnAlaProGlyLysGly 169

QY 610 CTGAGATGGGCTGAGCTTATATCATATGATGGAAGCACTAAATACTAGCAGACTCCGTG 669
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 170 LeuGlnTrrValSerAlaIleThrTrrPansSerGlyHisIleAspTyrAlaAspSerVal 189

QY 670 AAGGGCCGATTCACCATCTCCAGAGACATTCGAGAGACAGGTGTATCTAAATGAGAC 729
    ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|  ::::|
Db 190 GlnGlyArgPheThrIleSerArgAspAsnAlaIyAsnSerleuTyrleuGlnMetAsn 209

QY 730 AGCCTGAGAACTGAGGACACGGGCTGTCTATTACTGTGCGAGAGATCAGAGCCGTGGGT 789
```

```
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 210 SerleuAlaGluAspThrAlaValTrrTyrCysAlaIySValSerTyrleu----- 227

QY 790 GACTATGACCACTACTACGTTTGGACGTCCTGGGGCAAGGAGCACCGGTCCCGTCTCC 849
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 228 -----SerThrAlaSerSerleuAspTyrTrrGlyGlnGlyThrleuValThrValSer 245

QY 850 TCAGGATCCGAACAAAACTGATCAGCGAAGAGATCGAACCATCACCATCACCAT 906
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 246 Ser-----HisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 252
```

Search completed: February 18, 2005, 08:54:37  
Job time : 209 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2005, 08:45:58 ; Search time 82 Seconds  
(without alignments)  
1898,440 Million cell updates/sec

Title: US-09-194-164-14  
Perfect score: 1562  
Sequence: 1 EFMKKTALVALAGPATV.....GSEOKLISEEDLNHHHKL 304

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03: \*  
1: uniprot\_prot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688	43.5	262	2	Q65Z11 mus musculus
2	555	35.1	236	2	Q6P5S8
3	548	34.6	236	2	Q6P1L8
4	547.5	34.6	235	2	Q6GMV9
5	544.5	34.4	235	2	Q6PUF2
6	530	33.5	109	2	Q9UL78
7	526	33.2	129	1	KV3L_HUMAN
8	523	33.1	109	1	KV3B_HUMAN
9	520	32.9	129	1	KV3M_HUMAN
10	515.5	32.6	613	2	Q8WUK1
11	510	32.2	109	1	KV3E_HUMAN
12	506	32.0	109	1	KV3E_HUMAN
13	506	32.0	240	2	Q65ZC9
14	498.5	31.5	122	1	HV3G_HUMAN
15	497	31.4	109	2	Q9UL86
16	493	31.0	116	2	Q9UL93
17	491	31.0	109	1	KV3G_HUMAN
18	486.5	30.8	147	2	Q9Y5O9
19	484	30.6	108	1	KV3A_HUMAN
20	480	30.3	113	2	Q9UL90
21	478	30.2	478	2	Q6P1L8
22	475	30.0	472	2	Q6N089
23	473.5	29.9	573	2	Q8WU38
24	470	29.7	100	1	KV3C_HUMAN
25	468.5	29.6	235	2	Q6GMW0
26	467.5	29.6	606	2	Q6GMV2
27	466	29.5	236	2	Q6P1H7
28	463.5	29.3	122	1	HV3H_HUMAN
29	463.5	29.3	544	2	Q6P395
30	463	29.3	121	1	HV3J_HUMAN
31	458.5	29.0	122	2	Q9UL84

32	457	28.9	597	2	Q96BB9	Q96BB9 homo sapien
33	455	28.8	119	1	HV3I_HUMAN	P01770 homo sapien
34	455	28.8	121	2	Q9UL71	Q9UL71 homo sapien
35	454	28.7	109	2	Q9UL85	Q9UL85 homo sapien
36	451	28.5	493	2	Q8NCL6	Q8NCL6 homo sapien
37	449.5	28.4	128	1	KV3K_HUMAN	P06311 homo sapien
38	449	28.4	109	1	KV3F_HUMAN	P01624 homo sapien
39	449	28.4	493	2	Q6GCN4	Q6GCN4 homo sapien
40	448.5	28.4	126	1	HV3K_HUMAN	P01772 homo sapien
41	448	28.3	129	1	KV3H_HUMAN	P04207 homo sapien
42	445	28.1	464	2	Q6MZU6	Q6MZU6 homo sapien
43	444	28.1	470	2	Q6P3A4	Q6P3A4 homo sapien
44	443	28.0	519	2	Q6N092	Q6N092 homo sapien
45	442	27.9	589	2	Q7Z351	Q7Z351 homo sapien

## ALIGNMENTS

RESULT 1	ID	Q65Z11	PRELIMINARY;	PRT;	262 AA.
AC	Q65Z11;				
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)				
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)				
DB	Anti-HIV-1 reverse transcriptase single-chain variable.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Mus.				
OX	NCBI_Taxid=10090;				
RP	(1)				
RC	SEQUENCE FROM N.A.				
RX	TISUE=Hybridoma; PubMed=8648670;				
RA	Shahen F., Duan L., Zhu M., Bagasara O., Pomerantz R.J.;				
RT	"Targeting human immunodeficiency virus type 1 reverse transcriptase by intracellular expression of single-chain variable fragments to inhibit early stages of the viral life cycle.";				
RL	J. Virol. 70:3392-3400(1996).				
DR	EMBL; U48716; AB64342.1; -				
DR	GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.				
DR	InterPro; IPR003599; IG_1.				
DR	InterPro; IPR007110; IG_1like.				
DR	InterPro; IPR003598; IG_C2.				
DR	InterPro; IPR003596; IG_V.				
DR	Pfam; PF00047; IG_2.				
DR	SMART; SM00409; IG_2.				
DR	SMART; SM00408; IGC2; 2.				
DR	PROSITE; PS50835; IG_LIKE; 2.				
KW	RNA-directed DNA polymerase.				
SO	SEQUENCE 262 AA; 27842 MW; 7DF20138E53865B4 CRC64;				
Query Match	43.5%;	Score 688;	DB 2;	Length 262;	
Beet Local Similarity	51.4%;	Pred. No. 1.6e-44;			
Matches 142;	Conservative 44;	Mismatches 60;	Indels 30;	Gaps 6;	
QY	24	DIVLQSGTSLSPGERATLSCRASQSVSSYLAWYQKPGCAPRLLYGASTRATGMP	83		
DB	2	DIIMQSPATLSVTGDRVSLSCRASQSI-SDFLMYQKSHESRLLIKVSQSISSGTP	60		
QY	84	DRFSGSGGTDTLTLSRLPEDFAVYVYCOQYGSAPQPTQITFGGATKVEIKRTVAAPSV	143		
DB	61	SRFSGSGSGDPTLSINSVEPEDVGVYVYCOQNHSPF-LTFGAGTKLELRADAAPTV	116		
QY	144	S-----CGGSGGGGGGGGG-----SQVQLVESGGGVQGRSRLSCAASGPF	188		
DB	117	SIFPPSSKLGPGGSGGGSGGGSELGRSSVQLQESGSPSLVKKPSQTLISLTCSVTGDSI	176		
QY	169	RSFAMHWROALGKLEWAVAVSYDGTSTKYADSVKGRFTTSRDPSKNTVYVYKMSLRAT	248		
DB	177	TSGYNNWIRKPKGNKLDYMGVINYSGDI-YVNPISLKSNIISTADISKQYVYQLNLSVTTE	235		

QY 249 DRAVYICARDQSLIDYHYGLDWMGKTTTVSS 284  
 DB 236 DAATYCGGGLR-----MDYWGQGTSTVSS 262

RESULT 2  
 ID 06P58 PRELIMINARY; PRT; 236 AA.  
 AC 06P58;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxId=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Glandular pool- thyroid;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Glandular pool- thyroid;  
 RC Strausberg R.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 DR HSSP; BC062704; AAH62704.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG\_2.  
 DR SMART; SM00407; IG\_C1; 1.  
 DR InterPro; IPR003596; IG\_V.  
 DR InterPro; IPR003597; IG\_C1.  
 DR SMART; SM00409; IG\_2.  
 DR SMART; SM00407; IG\_C1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25773 MW; 953E37BB4FF5F27 CRC64;

Query Match 35.1%; Score 555; DB 2; Length 236;  
 Best Local Similarity 57.8%; Pred. No. 2e-34;  
 Matches 126; Conservative 18; Mismatches 48; Indels 26; Gaps 6;

QY 24 DIVTQSPGTLSPGERATLSCRAQGVSSSYLAWYQKPGQAPRLIYGASTRATGMP 83  
 DB 21 EIVTQSPGTLSPGERATLSCRAQGVSSSYLAWYQKPGQAPRLIYGASTRATGMP 80  
 QY 84 DRFGSGSGCTDFTLTITLRLPEDFAVYFCQQYGTG---PSLTFGGGTRVEIKRTVAAPSV 143

DB 81 DRFGSGSGCTDFTLTITLRLPEDFAVYFCQQYGTG---PSLTFGGGTRVEIKRTVAAPSV 137  
 QY 144 SGGGSGGGGSGGGGSGGVVQPGSRILSLSCAASGPPRRPAMHW-VROALGK 202  
 DB 138 -----RFPSPDEQLKSGTASV-----CLNNFYREAKVQKVNALLOS 178

QY 203 GLEWVAIVSYDSTYKYVADSVKGRFTISR-DTSKNTVY 239  
 DB 179 GNSQSVTEQDSKDSSTY--SLSTLTLSKADYERKRVY 214

RESULT 3  
 ID 06P18 PRELIMINARY; PRT; 236 AA.  
 AC 06P18;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxId=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Brain;  
 RC Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR HSSP; BC032451; AAH32451.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG\_2.  
 DR SMART; SM00407; IG\_C1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25834 MW; 66479A877A3C0053 CRC64;

Query Match 34.6%; Score 548; DB 2; Length 236;  
 Best Local Similarity 58.8%; Pred. No. 6.8e-34;  
 Matches 127; Conservative 14; Mismatches 49; Indels 26; Gaps 6;

QY 26 VLTQSPGTLSPGERATLSCRAQGVSSSYLAWYQKPGQAPRLIYGASTRATGMPDR 85



```

DB 23 VLTGPGTILSLSPGERATILSCRASQSLSSYLAWYQKQAPRLITVSSRATGTPR 82
QY 86 FSGSGSGTDFTLTILSRLEPEDPAVYVYCOQYSSPQPTQITFGGCTKVEIKRTVAAPSV 145
DB 83 FSGSGSGTDFTLTILSRLEPEDPAVYVYCOQYSS---RPITFGGCTKVEIKRTVAAPSV-- 137
QY 146 GGGSGSGSGGSGGSGQVQVYVSGGQVYVQPGSLRLSCASGPPRPFAMMW-VQALGKGL 204
DB 138 -----FIPPPSDEQLKSGTASV-----CLNNFYPREAKVQMKVDNALQSGN 180
QY 205 EMWAVISYDGSSTKYVADSVKGRFTISR-DTSKNYV 239
DB 181 SOESVTEQDSKDY--SLSTLTLSKADYEKHKV 214

RESULT 4
Q6GMV9 PRELIMINARY; PRT; 235 AA.
AC 06GMV9;
DB 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
OS Hypothetical protein.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cavalet T.L., Scheetz T.E.,
RA Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DB EMBL; BC073793; AAH73793.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-seel; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

```

```

Query Match 34.6%; Score 547.5; DB 2; Length 235;
Best Local Similarity 57.8%; Pred. No. 7,4e-34;
Matches 126; Conservative 15; Mismatches 50; Indels 27; Gaps 6;

QY 24 DIVLQSPCTLSLSPGERATILSCRASQSSSYLAWYQKQAPRLITVSSRATGTPR 83
DB 21 EIVLQSPCTLSLSPGERATILSCRASQSSSYLAWYQKQAPRLITVSSRATGTPR 80
QY 84 DRFGSGSGTDFTLTILSRLEPEDPAVYVYCOQYSSPQPTQITFGGCTKVEIKRTVAAPSV 143
DB 81 DRFGSGSGTDFTLTILSRLESEDPAVYVYCOQYSSPQPTQITFGGCTKVEIKRTVAAPSV 136
QY 144 SGGSGSGSGGSGGSGQVQVYVSGGQVYVQPGSLRLSCASGPPRPFAMMW-VQALGK 202
DB 137 -----FIPPPSDEQLKSGTASV-----CLNNFYPREAKVQMKVDNALQSGN 177
QY 203 EMWAVISYDGSSTKYVADSVKGRFTISR-DTSKNYV 239
DB 178 GNSQSVTEQDSKDY--SLSTLTLSKADYEKHKV 213

RESULT 5
Q6UPF2 PRELIMINARY; PRT; 235 AA.
AC 06UPF2;
DB 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
OS Hypothetical protein.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cavalet T.L., Scheetz T.E.,
RA Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL; BC016380; AAH16380.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-seel; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.

```

DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.

SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 34.4%; Score 544.5; DB 2; Length 235;  
 Best Local Similarity 58.3%; Pred.No.1.3e-33;  
 Matches 127; Conservative 15; Mismatches 49; Indels 27; Gaps 6

QY	24	DIVLTQSCTSLISGERATLSCRASQSVSSSYLAMVQQKQAQRLLIYGASTATGMP	83
DB	21	EIVLQSPATLSLSGERATLSCRASQIVSSAYLAMVQKPQAARLLMFGSSSRATGIP	80
QY	84	DRFSGSGGTFTLTISRLEPEDFAVVYCCQGSSPQTPTLFGGTVKRIKRTVAASV	143
DB	81	DRFSGSGGTFTLTISRLEPEDFAVVYCCQGSS---QGFPGTITVDIKRTVAASV	136
QY	144	SGGGSGGGSGGGSGGVQLVBSGGGVQPGRSLRLSCAAGFPFRSAMHW-VRAIGK	202
DB	137	-----FIPEPDQLSKGTASV-----CLNNFYREAKVQMKNALQS	177
QY	203	GLEWVAIVSYDSTKYADSVKGRFTISR-DTSKNTVY	239
DB	178	GNSGSVTEDPSKDSTY--SLSTITLSKADYEKKAVY	213

RESULT 6

Q9UL78	PRELIMINARY;	PRT;	109 AA.
ID	Q9UL78		
AC	Q9UL78;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DI	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-MAY-2004 (TREMBLrel. 26, last annotation update)		
DE	Myosin-reactive Immunoglobulin light chain variable region (Fragment).		
DE	Homo sapiens (Human).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;		
RA	Yu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;		
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";		
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).		
DR	EMBL; AF035036; AAD56272.1; -.		
DR	PIR; A30601; A30601.		
DR	PIR; A30608; A30608.		
DR	PIR; A30601; B30601.		
DR	PIR; B30607; B30607.		
DR	PIR; C30601; C30601.		
DR	PIR; C30607; C30607.		
DR	PIR; C30608; C30608.		
DR	PIR; D30601; D30601.		
DR	PIR; D30607; D30607.		
DR	PIR; D30608; D30608.		
DR	PIR; D30607; H30607.		
DR	PIR; H30608; H30608.		
DR	PIR; H44151; H44151.		
DR	PIR; I30601; I30601.		
DR	PIR; PH0963; PH0963.		
DR	PIR; PH0964; PH0964.		
DR	PIR; PH0965; PH0965.		
DR	PIR; S33988; S33988.		
DR	PIR; S34096; S34096.		
DR	HSSF; P01625; IEX3.		
DR	Interpro; IPRO07110; Ig-like.		

[illegible]

```

Db      21 EIVLQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLILYGASRATGIP 80
Oy      84 DRFGSSGSGTDTLTISRLEPDPFVAVYCCQYGGSSPQTPIFGGKTKEIKR 136
Db      81 DRFGSSGSGTDTLTISRLEPDPFVAVYCCQYGGSSPQTPIFGGKTKEIKR 129

RESULT 8
KV3B_HUMAN
ID      KV3B_HUMAN      STANDARD; PRT; 109 AA.
AC      P01620;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DS      Ig kappa chain V-II region SI.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=82046598; PubMed=6794615;
RA      Andrews D.W., Capra J.D.;
RT      "Amino acid sequence of the variable regions of light chains from two
RT      idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
RT      group."
RL      Biochemistry 20:5816-5822(1981).
RC      -1- MISCELLANEOUS: This chain was isolated from an Igm with anti-gamma
CC      globulin activity.
DR      PIR: A01892; KAHUSI.
DR      HSP: P01625; IIVE.
DR      GO: GO:0005576; C:extracellular; NAS.
DR      GO: GO:0003823; F:antigen binding; NAS.
DR      GO: GO:0006955; P:immune response; NAS.
DR      InterPro: IPR007110; Ig-like.
DR      InterPro: IPR003596; Ig_v.
DR      Pfam: PF00047; Ig_1.
DR      SMART, SM00406; IGV; 1.
DR      PROSITE, PS50835; IG_LIKE; 1.
KW      Direct protein sequencing; Immunoglobulin V region.
FT      DISULFID 23 89
FT      NON TER 109 109
SQ      SEQUENCE 109 AA; 11775 MW; 7689C3BCD646FFB4 CRC64;

Query Match 33.1%; Score 523; DB 1; Length 109;
Best Local Similarity 90.3%; Pred. No. 2, 2e-32;
Matches 102; Conservative 6; Mismatches 1; Indels 4; Gaps 1;

Oy      24 DIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLILYGASRATGIP 83
Db      1 EIVLQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLILYGASRATGIP 60

Oy      84 DRFGSSGSGTDTLTISRLEPDPFVAVYCCQYGGSSPQTPIFGGKTKEIKR 136
Db      61 DRFGSSGSGTDTLTISRLEPDPFVAVYCCQYGGSSPQTPIFGGKTKEIKR 109

RESULT 9
KV3M_HUMAN
ID      KV3M_HUMAN      STANDARD; PRT; 129 AA.
AC      P18136;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      15-JUN-1999 (Rel. 38, Last annotation update)
DS      Ig kappa chain V-III region HIC precursor.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=86171307; PubMed=3127527;
RA      Kippes T.J., Tomhave E., Chen P.P., Carson D.A.;

```

```

RT      "Autoantibody-associated kappa light chain variable region gene
RT      expressed in chronic lymphocytic leukemia with little or no somatic
RT      mutation. Implications for etiology and immunotherapy."
RL      J. Exp. Med. 167:840-852(1988).
CC      -1- DISBASE: The protein is one of the surface immunoglobulin M
CC      autoantibodies expressed in patients with chronic lymphocytic
CC      leukemia.
DR      PIR: P10021; KAHUHI.
DR      HSP: P01625; IIEQ.
DR      GO: GO:0005576; C:extracellular; NAS.
DR      GO: GO:0003823; F:antigen binding; NAS.
DR      GO: GO:0006955; P:immune response; NAS.
DR      InterPro: IPR007110; Ig-like.
DR      InterPro: IPR003596; Ig_v.
DR      Pfam: PF00047; IGV; 1.
DR      SMART, SM00406; IGV; 1.
DR      PROSITE, PS50835; IG_LIKE; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL 1 20
FT      CHAIN 21 129
FT      DOMAIN 21 43
FT      DOMAIN 44 55
FT      DOMAIN 56 70
FT      DOMAIN 71 77
FT      DOMAIN 78 109
FT      DOMAIN 110 118
FT      DOMAIN 119 129
FT      DISULFID 43 109
FT      NON TER 129 129
SQ      SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 32.9%; Score 520; DB 1; Length 129;
Best Local Similarity 91.2%; Pred. No. 4, 6e-32;
Matches 103; Conservative 3; Mismatches 3; Indels 4; Gaps 1;

Oy      24 DIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLILYGASRATGIP 83
Db      21 EIVLQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLILYGASRATGIP 80

Oy      84 DRFGSSGSGTDTLTISRLEPDPFVAVYCCQYGGSSPQTPIFGGKTKEIKR 136
Db      81 DRFGSSGSGTDTLTISRLEPDPFVAVYCCQYGGSSPQTPIFGGKTKEIKR 129

RESULT 10
O8WUK1
ID      O8WUK1          PRELIMINARY; PRT; 613 AA.
AC      O8WUK1;
DT      01-MAR-2002 (TRMBLrel. 20, Created)
DT      01-MAR-2002 (TRMBLrel. 20, Last sequence update)
DT      01-MAR-2004 (TRMBLrel. 26, Last annotation update)
DS      IGHM protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      TISSUE=Primary B-Cells;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Mariani B., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ueda T.B., Tomshyuk S., Carninci P., Prange C.,
RA      Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahy J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

```

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzyzanski M.I., Skolake J., Smalins D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Maitra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SOURCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.,  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC020240; AA020240.1; -.  
DR PIR; F36005; F36005.  
DR PIR; G36005; G36005.  
DR PIR; PH1642; PH1642.  
DR PIR; PH1643; PH1643.  
DR PIR; PH1645; PH1645.  
DR PIR; PH1646; PH1646.  
DR PIR; PL0098; PL0098.  
DR PIR; PL0120; PL0120.  
DR PIR; S15590; S15590.  
DR PIR; S31116; S31116.  
DR PIR; S31119; S31119.  
DR PIR; S70442; S70442.  
DR HSP; P01861; IADQ.  
DR Pfam; PF07654; Cl-sef; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN; 3.  
SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;  
  
Query Match 32.6%; Score 515.5; DB 2; Length 613;  
Best Local Similarity 79.5%; Pred. No. 6.2e-31;  
Matches 101; Conservative 7; Mismatches 14; Indels 5; Gaps 1;  
  
QY 160 QVQLVSGGQVQPGKSLRLSCAASGFPSPRFAMHWVRQALGKLEWVAIVSDGSTKY 219  
DB 20 QVQLVSGGQVQPGKSLRLSCAASGFTPSYGMHWVRQAPKGLKLEWVAIVSDGSKYY 79  
QY 220 ADSVGRFTISRDTSKNTYYLKMSIRTDIAVYYCARQOSLGDYDHYGADVWGKTT 279  
DB 80 ADSVGRFTISRDTSKNTYYLKMSIRTDIAVYYCARQOSLGDYDHYGADVWGKTT 134  
QY 280 VTVSSGS 286  
DB 135 VTVSSGS 141  
  
RESULT 11  
KV3D HUMAN STANDARD; PRT; 109 AA.  
ID KV3D HUMAN  
AC P01623;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-II region Tl.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OK NCBI\_taxonomy=9606;  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=72188439; PubMed=5027703;  
RA Suter L., Barikol H.U., Matanbe S., Hilschmann N.,  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein  
RT Tl). IV. The complete amino acid sequence and its significance for the  
RT mechanism of antibody production.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).  
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
DR PIR; A01895; K3HUT1.

DR HSP; P01625; ILVE.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DISULFID 23 89  
FT NON\_TER 109 109  
SQ SEQUENCE 109 AA; 11746 MW; 8C35058C0C77499C CRC64;  
  
Query Match 32.2%; Score 510; DB 1; Length 109;  
Best Local Similarity 88.5%; Pred. No. 2.2e-31;  
Matches 100; Conservative 6; Mismatches 3; Indels 4; Gaps 1;  
  
QY 24 DIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYGASTRATMP 83  
DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYVAASRATGP 60  
QY 84 DRFGSGSGTPTLTISRLPEDEPAVYVYCCQYGSPPQITPFGSGTKVEIKR 136  
DB 61 DRFGSGSGTPTLTISRLPEDEPAVYVYCCQYGSPPS---TFQGTKEVLEIKR 109  
  
RESULT 12  
KV3E HUMAN STANDARD; PRT; 109 AA.  
ID KV3E HUMAN  
AC P01623;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-II region WOL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OK NCBI\_taxonomy=9606;  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=82046598; PubMed=6794615;  
RA Andrews D.W., Capra J.D.,  
RT "Amino acid sequence of the variable regions of light chains from two  
RT idiosyncratically cross-reactive human Igm anti-gamma-globulins of the Wa  
RT group.";  
RL Biochemistry 20:5816-5822(1981).  
CC -I- MISCELLANEOUS: This chain was isolated from an Igm with anti-gamma  
CC globulin activity.  
DR PIR; A01896; K3HUTL.  
DR HSP; P01625; ILVE.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin V region.  
FT DISULFID 23 89  
FT NON\_TER 109 109  
SQ SEQUENCE 109 AA; 11746 MW; 566C1156B9CBEE CRC64;  
  
Query Match 32.0%; Score 506; DB 1; Length 109;  
Best Local Similarity 88.5%; Pred. No. 4.4e-31;  
Matches 100; Conservative 4; Mismatches 5; Indels 4; Gaps 1;  
  
QY 24 DIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYGASTRATMP 83  
DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYGAASRATGP 60

QY 84 DRFGSSGCTPDLTISRLEPPDPVYVCOYGSPPQTPIFGGKTVEIKR 136  
 DB 61 DRFGSSGCTPDLTISRLEPPDPVYVCOYGSPPQTPIFGGKTVEIKR 109

## RESULT 13

Q65ZC9 PRELIMINARY; PRT; 240 AA.  
 AC Q65ZC9;  
 DT 25-OCT-2004 (TREMBLrel. 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Single-chain Fv (Fragment).  
 GN Name=SCFV;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C1q/7;  
 RX MEDLINE=97362799; PubMed=9219263;  
 RA Kontermann R.E., Wing M.G., Winter G.;  
 RT "Complement recruitment using bispecific diabodies";  
 RL Nat. Biotechnol. 15:629-631(1997).  
 DR EMBL; Y13056; CAA73499.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IG; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 32.0%; Score 506; DB 2; Length 240;  
 Best Local Similarity 80.2%; Pred. No. 1.1e-30;  
 Matches 101; Conservative 5; Mismatches 12; Indels 8; Gaps 2;

QY 160 QVQLVSGGCVVQPSRSLRSCAAGFPFRSFMHWVRQALGKLEWVAIVISDGSTKY 219  
 DB 1 QVQLVSGGCVVQPSRSLRSCAAGFPFRSFMHWVRQALGKLEWVAIVISDGSTKY 60  
 QY 220 ADSVKGRTISRDTSKNTVYLLKNSLRTEDTAVYVYCARQDLSGPDHYGADVWGKGT 279  
 DB 61 ADSVKGRTISRDTSKNTVYLLKNSLRTEDTAVYVYCARQDLSGPDHYGADVWGKGT 112  
 QY 280 VTSSG 285  
 DB 113 VTSSG 118

## RESULT 14

Q65ZC9 PRELIMINARY; PRT; 122 AA.  
 AC Q65ZC9;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig heavy chain V-III region CAM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=81013859; PubMed=6774332;  
 RA Lehman D.W., Putnam F.W.;  
 RT "Amino acid sequence of the variable region of a human mu chain:  
 location of a possible JH segment.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).

CC -1- MISCELLANEOUS: This mu chain was isolated from the plasma of a  
 CC patient with macroglobulinemia.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02051; M3HUM.  
 DR HSSP; P01772; 2PB4.  
 DR GO; GO:0005576; Cxcracellular; NAS.  
 DR GO; GO:0003823; F; antigen binding; NAS.  
 DR GO; GO:0006955; P; immune response; NAS.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region;  
 KW Pyroliidone carboxylic acid.  
 FT DOMAIN 1 112  
 FT MOD\_RES 1 1  
 FT NON\_TER 122  
 SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 31.5%; Score 498.5; DB 1; Length 122;  
 Best Local Similarity 74.4%; Pred. No. 1.9e-30;  
 Matches 93; Conservative 15; Mismatches 14; Indels 3; Gaps 1;

QY 160 QVQLVSGGCVVQPSRSLRSCAAGFPFRSFMHWVRQALGKLEWVAIVISDGSTKY 219  
 DB 1 QVQLVSGGCVVQPSRSLRSCAAGFPFRSFMHWVRQALGKLEWVAIVISDGSTKY 60  
 QY 220 ADSVKGRTISRDTSKNTVYLLKNSLRTEDTAVYVYCARQDLSGPDHYGADVWGKGT 279  
 DB 61 ADSVKGRTISRDTSKNTVYLLKNSLRTEDTAVYVYCARQDLSGPDHYGADVWGKGT 117  
 QY 280 VTSSG 284  
 DB 118 VTSSG 122

## RESULT 15

Q9UL86 PRELIMINARY; PRT; 109 AA.  
 AC Q9UL86;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin kappa chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.";  
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035028; AAD56264.1; -.  
 DR PIR; B30607; B30607.  
 DR PIR; B30601; B30601.  
 DR HSSP; P01625; 1EK3.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003596; IG\_V.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 109  
 SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DACC83 CRC64;

Query Match 31.4%; Score 497; DB 2; Length 109;  
 Best Local Similarity 87.6%; Pred. No. 2.2e-30;  
 Matches 99; Conservative 4; Mismatches 6; Indels 4; Gaps 1;

**Tue Feb 22 09:00:47 2005**

us-09-194-164-14.rup

**Page 8**

[illegible]

Search completed: February 18, 2005, 08:57:28  
Job time : 83 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2005, 08:42:23 ; Search time 81 Seconds  
(without alignments)  
1451.545 Million cell updates/sec

Title: US-09-194-164-14

Perfect score: 1582  
Sequence: 1 EFMKKTATATVVALAGPATV.....GSEQKLTSEBDLNHHHKL 304

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 366760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_16Dec04:\*

1: geneseqp19808:\*\n2: geneseqp19908:\*\n3: geneseqp20008:\*\n4: geneseqp20018:\*\n5: geneseqp20028:\*\n6: geneseqp20038:\*\n7: geneseqp20048:\*\n8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1582	100.0	304	AAW40070	AAW40070 Human H11
2	1582	100.0	304	AAE00947	AAE00947 Human mon
3	1582	100.0	304	ABU10486	ABU10486 C-antigen
4	1582	100.0	304	ADO52296	ADO52296 Human ant
5	1460.5	92.3	287	AAW40071	AAW40071 Human H11
6	1460.5	92.3	287	AAE00948	AAE00948 Human mon
7	1460.5	92.3	287	ABU10487	ABU10487 C-antigen
8	1460.5	92.3	287	ADO52299	ADO52299 Human ant
9	1016.5	64.3	638	ADA89103	ADA89103 Phage dis
10	1016.5	64.3	638	ADA90139	ADA90139 Anti-Abet
11	1016.5	64.3	638	ADA91410	ADA91410 Anti-Abet
12	1016.5	64.3	747	ADG74355	ADG74355 MSPRO lig
13	986	62.3	523	AAI44494	AAI44494 HD70bcFv-
14	986	62.3	524	AAI44495	AAI44495 HD70bcFv-
15	972.5	61.5	628	ABJ38670	ABJ38670 Fab expre
16	961.5	60.8	252	ADO58062	ADO58062 S2 cell d
17	928	58.7	352	AAV06272	AAV06272 Anti-Fc g
18	916.5	57.9	295	ABG68848	ABG68848 C219scFv
19	914	57.8	490	AAI56637	AAI56637 hCART bin
20	892	55.4	283	AAU75160	AAU75160 Kabat con
21	892	55.4	283	ABG73148	ABG73148 Kabat con
22	892	55.4	283	ABG73148	ABG73148 Kabat con
23	891.5	55.4	319	ABG68851	ABG68851 Interfero
24	887	56.1	263	AAW97889	AAW97889 Kabat con
25	866.5	54.8	630	ADF69023	ADF69023 Chlotopia

26	866.5	54.8	639	7	ADF68991	ADF68991 Chlotopia
27	865	54.7	334	3	AAI82515	AAI82515 Anti-HA p
28	863.5	54.6	277	7	ADF69018	ADF69018 Human chl
29	858.5	54.3	250	8	AD161980	AD161980 Human scF
30	857.5	54.2	279	7	ABR61568	ABR61568 HIV-1 neu
31	849.5	53.7	252	8	ADO40405	ADO40405 Single ch
32	849.5	53.7	252	8	ADO40409	ADO40409 Single ch
33	849.5	53.7	253	8	ADO40406	ADO40406 Single ch
34	849.5	53.7	254	8	ADO40412	ADO40412 Single ch
35	847	53.5	239	8	ADO40413	ADO40413 Single ch
36	846.5	53.5	484	6	ABR55341	ABR55341 Amino aci
37	840	53.1	247	7	ADC03132	ADC03132 Colon spe
38	834.5	52.7	254	8	ADG17470	ADG17470 HIV envel
39	828.5	52.4	487	8	ADG17475	ADG17475 HIV envel
40	828	52.3	650	6	ABR62591	ABR62591 Anti-CD7
41	828	52.3	651	6	ABR62590	ABR62590 Anti-CD7
42	824.5	52.1	247	8	ADO40408	ADO40408 Single ch
43	824.5	52.1	254	8	ADG17468	ADG17468 HIV envel
44	824	52.1	443	6	ABG76488	ABG76488 Humanised
45	824	52.1	443	6	ABG74240	ABG74240 ChimERIC

## ALIGNMENTS

RESULT 1  
AAW40070 ID AAW40070 standard; protein; 304 AA.  
XX AC AAW40070;  
XX DT 29-MAY-1998 (first entry)  
XX DE Human H11-scFv construct monomer forming protein.  
XX KW H11; monoclonal antibody; Mab; C-antigen; variable region heavy chain;  
XX KW V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe;  
XX KW primer; vaccine; gene therapy; glioblastoma; neuroblastoma;  
XX KW malignant melanoma; adenocarcinoma; small cell lung carcinoma;  
XX KW single chain variable region; scFv.  
XX OS Synthetic.  
XX OS Homo sapiens.  
XX PN WO9744461-A2.  
XX PD 27-NOV-1997.  
XX PF 22-MAY-1997; 97WO-US008962.  
XX PR 22-MAY-1996; 96US-00657449.  
XX PA (NOVO-) NOVOPHARM BIOTECH INC.  
XX PI Dan MD, Maiti PK, Kaplan HA;  
XX DR WPI, 1998-018515/02.  
XX DR N-PSDB; AAV10118.  
XX PT Antigen binding fragment from monoclonal antibody, H11 - allows tumour  
XX PT specific detection and treatment of neoplasia.  
XX PS Claim 5; Page 92-93; 126pp; English.  
XX CC This sequence represents a human H11 monoclonal antibody single chain V  
XX CC region fragment (H11-scFv) construct which is capable of forming  
XX CC monomers. This construct is used to determine the ability of H11-scFv  
XX CC antibody fragments to bind specifically to the C-antigen on cancer cells.  
XX CC Such antigen binding fragments may be used for treating a patient with  
XX CC neoplasia. It is especially useful in the detection of lymphomas and  
XX CC leukemias where the tumour cells bearing the C antigen are circulating  
XX CC in the patients bloodstream. The polynucleotide sequence may be used as a  
XX CC primer or a probe and the encoded protein may be used in a vaccine or for

CC gene therapy. The human monoclonal antibody (MAb), designated H11,  
CC specifically recognizes cancerous cells. H11 is specific for  
CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,  
CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and  
CC prostate adenocarcinoma  
XX  
SQ Sequence 304 AA;

Query Match 100.0%; Score 1582; DB 2; Length 304;  
Best Local Similarity 100.0%; Pred. No. 3.6e-102;  
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFMKKTALAIYALAGFATVAQADIVLTOSPGTSLSPGERATLSCASQSVSSSYLAWY 60  
DB 1 EFMKKTALAIYALAGFATVAQADIVLTOSPGTSLSPGERATLSCASQSVSSSYLAWY 60  
QY 61 QOKRGAAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDPAVYYCCQYGSPPQ 120  
DB 61 QOKRGAAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDPAVYYCCQYGSPPQ 120  
QY 121 TPQITFGGTVKVEIKRTVAAPSVVGGGSGGSGGVQVLESQGVVQPGRLRLS 180  
DB 121 TPQITFGGTVKVEIKRTVAAPSVVGGGSGGSGGVQVLESQGVVQPGRLRLS 180  
QY 181 CAASGPPFRSFAMHWVQALGKLEWYAVISYDSTKYVADSVKGRFTISRDTSKNTYYL 240  
DB 181 CAASGPPFRSFAMHWVQALGKLEWYAVISYDSTKYVADSVKGRFTISRDTSKNTYYL 240  
QY 241 KMSLRTEDTAVYYCARDQSLGDYHYGLDVGKGTITVVSQSGEQKLISEEDLNHHH 300  
DB 241 KMSLRTEDTAVYYCARDQSLGDYHYGLDVGKGTITVVSQSGEQKLISEEDLNHHH 300  
QY 301 HHKL 304  
DB 301 HHKL 304

## RESULT 2

AAE00947 ID AAE00947 standard; protein; 304 AA.

XX AAE00947;  
DE 04-JUL-2001 (first entry)

XX Human monoclonal antibody H11-single chain variable region (scFv) #1.

KW Human; monoclonal antibody; Mab; H11; single chain variable region; scFv;  
KW neoplastic disease; melanoma; immunoglobulin IgM; gene therapy; lymphoma;  
KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;  
KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;  
KW C-antigen; chronic leukemia; glioma.

XX Homo sapiens.

XX Key Location/Qualifiers  
XX Region 144..158  
XX FT /label= Linker

XX FT Misc-difference 302..303  
XX FT /note="Encoded by CATTAGTAAAG"

XX US6207153-B1.

XX 27-MAR-2001.

XX 22-MAY-1997; 97US-00862124.

XX 22-MAY-1996; 96US-00657449.

XX (VIVE-) VIVENTIA BIOTECH INC.

XX Dan MD, Maith PK, Kaplan HA;

DR WPI; 2001-289584/30.  
DR N-PSDB; AAD04537.

XX Composition comprising antigen binding fragments of an antibody that  
PT recognizes an antigen on neoplastic cells but not on normal cells for use  
PT in diagnosis, imaging and treatment of carcinomas.

XX Claim 1; Col 63-66; 56pp; English.

XX The present sequence is human monoclonal antibody (Mab), H11-single chain  
CC variable region (scFv). The H11 light chain variable region is linked to  
CC the heavy chain variable region through a (SGGGG)3 linker to form  
CC monomers. The invention relates to human monoclonal antibody (Mab) H11,  
CC H11-(scFv) single chain variable (V) region fragment and their  
CC corresponding DNA molecules. H11 antibody is an immunoglobulin of IgM  
CC subclass which is specific to C-antigen found specifically on neoplastic  
CC cells and not on normal cells. H11 is an antibody obtained from the  
CC fusion of peripheral blood lymphocytes of a 64 year old male with a low  
CC grade glioma and fused to a human myeloma cell line to produce a  
CC hybridoma designated NBGM1/H11. A pharmaceutical composition comprising  
CC H11 and its derivatives are useful in the diagnosis, imaging and  
CC treatment of neoplastic disease, particularly, melanoma, breast  
CC carcinoma, lung carcinoma, ovarian carcinoma, colon carcinoma, gastric  
CC carcinoma, prostate carcinoma, lymphoma carcinoma, neuroblastoma, glioma,  
CC soft tissue sarcoma, small cell lung carcinoma, prostatic adenocarcinoma,  
CC B and T cell lymphomas and chronic leukemias. H11 DNA is also used in  
CC vaccines and gene therapy

SQ Sequence 304 AA;

Query Match 100.0%; Score 1582; DB 4; Length 304;  
Best Local Similarity 100.0%; Pred. No. 3.6e-102;  
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFMKKTALAIYALAGFATVAQADIVLTOSPGTSLSPGERATLSCASQSVSSSYLAWY 60  
DB 1 EFMKKTALAIYALAGFATVAQADIVLTOSPGTSLSPGERATLSCASQSVSSSYLAWY 60  
QY 61 QOKRGAAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDPAVYYCCQYGSPPQ 120  
DB 61 QOKRGAAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDPAVYYCCQYGSPPQ 120  
QY 121 TPQITFGGTVKVEIKRTVAAPSVVGGGSGGSGGVQVLESQGVVQPGRLRLS 180  
DB 121 TPQITFGGTVKVEIKRTVAAPSVVGGGSGGSGGVQVLESQGVVQPGRLRLS 180  
QY 181 CAASGPPFRSFAMHWVQALGKLEWYAVISYDSTKYVADSVKGRFTISRDTSKNTYYL 240  
DB 181 CAASGPPFRSFAMHWVQALGKLEWYAVISYDSTKYVADSVKGRFTISRDTSKNTYYL 240  
QY 241 KMSLRTEDTAVYYCARDQSLGDYHYGLDVGKGTITVVSQSGEQKLISEEDLNHHH 300  
DB 241 KMSLRTEDTAVYYCARDQSLGDYHYGLDVGKGTITVVSQSGEQKLISEEDLNHHH 300  
QY 301 HHKL 304  
DB 301 HHKL 304

RESULT 3  
ABU10486 ID ABU10486 standard; protein; 304 AA.

XX ABU10486;

XX 07-AUG-2003 (first entry)

XX C-antigen antibody H11 single chain variable region fragment #1.

KW Human; antibody; H11; single chain variable region; gene therapy; scFv;  
KW neoplasia; tumour; recurrence risk; C-antigen; melanoma; neuroblastoma;  
KW glioma; soft tissue sarcoma; small cell lung carcinoma; brain cancer;  
KW C-antigen specific antibody; alpha; cancer; vaccine.



```

XX OS Homo sapiens.
XX OS Synthetic.
XX PH Key
XX FT Misc-difference 302.303
XX FT /note="Encoded by CATTAGTGAAG"
XX PN US2003021779-A1.
XX PD 30-JAN-2003.
XX PF 13-FEB-2001, 2001US-00782397.
XX PR 22-MAY-1996; 96US-00657449.
XX PR 22-MAY-1997; 97US-00862124.
XX PA (DANM/) DAN M D.
XX PA (MATT/) MATTI P K.
XX PA (KAPL/) KAPLAN H A.
XX PI Dan MD, Maiti PK, Kaplan HA;
XX DR WPI: 2003-456278/43.
XX DR N-PSDB; ACA62168, ACA62169.
XX PT Novel antigen binding fragment of monoclonal antibody specific for
XX PT antigen detected on neoplastic cells, useful for diagnosing or treating
XX PT cancer, for manufacturing novel reagents and as diagnostic and imaging
XX PT reagent.
XX PS Claim 5; Page 34; 62pp; English.
XX CC The invention relates to a polypeptide which is an antigen binding
XX CC fragment of a monoclonal antibody specific for an antigen detected on
XX CC neoplastic cells. The antigen binding fragment (ABF) is useful for
XX CC treating a patient with a neoplasia. The individual has a clinically
XX CC detectable tumour. The method is useful for palliating the neoplasia. The
XX CC method reduces the risk of recurrence of a clinically detectable tumour.
XX CC The antigen binding fragment is labelled with a therapeutic moiety such
XX CC as radioisotopes or immunomodulators. ABF is useful for detecting C-
XX CC antigen in a sample. The polypeptide is useful for diagnosing, localising
XX CC and/or treating neoplasias, including melanoma, neuroblastoma, glioma,
XX CC soft tissue sarcoma and small cell lung carcinoma. The polypeptide is
XX CC useful for manufacturing novel reagents and for treating and imaging
XX CC brain cancer. ABF is useful as a diagnostic and imaging reagent. The
XX CC composition is useful for eliciting an immune response against neoplasia.
XX CC The polynucleotide is useful in expression systems for the production of
XX CC C-antigen specific antibody, termed H11 or alphaC, as hybridisation
XX CC probes to assay for the presence of alphaC polynucleotide or related
XX CC sequences in a sample, as primers to effect amplification of desired
XX CC polynucleotides and in pharmaceutical compositions including vaccines and
XX CC for gene therapy. The polynucleotide is also useful for genetically
XX CC altering cells in vitro, thus treating various types of cancer. The
XX CC polypeptide, polynucleotide and the composition are useful for detecting
XX CC or treating cancer, including therapy of cancer and prophylactic care,
XX CC particularly for decreasing the risk of recurrence. The present sequence
XX CC represents the amino acid sequence of the human C-antigen specific
XX CC antibody H11 single chain variable region fragment, scfv, #1
XX SS Sequence 304 AA:

```

```

Query Match 100.0%; Score 1582; DB 7; Length 304;
Best Local Similarity 100.0%; Pred. No. 3.6e-102;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 EEMKKTAAIIVAAAGFATVAQADIVLTQSPGTLSPSPERATLSCRAQSVSSTLAVY 60
DB 1 EEMKKTAAIIVAAAGFATVAQADIVLTQSPGTLSPSPERATLSCRAQSVSSTLAVY 60
QY 61 QOKPGQAPRLLIYGASTRATGMPDRPFGSGSGTDFLTISRLEPEDFAVYYCCQYQSSPQ 120
DB 61 QOKPGQAPRLLIYGASTRATGMPDRPFGSGSGTDFLTISRLEPEDFAVYYCCQYQSSPQ 120

```

```

QY 121 TPQITFGGCTKYEIKRTVAAPSVSGGGSGGGSGGVQLVBSGGGVVQPGSLRLS 180
DB 121 TPQITFGGCTKYEIKRTVAAPSVSGGGSGGGSGGVQLVBSGGGVVQPGSLRLS 180
QY 181 CAASGPPRPSFAMHWVRQALGKLEWNAVITYDGSRTKYADSVKGFRTISRTSKTYVL 240
DB 181 CAASGPPRPSFAMHWVRQALGKLEWNAVITYDGSRTKYADSVKGFRTISRTSKTYVL 240
QY 241 KMSLRTEBDTAVYYCARDQSLGDDYHYGLDPMWKGTTVTVSSGSEQKLISEEDLNHHH 300
DB 241 KMSLRTEBDTAVYYCARDQSLGDDYHYGLDPMWKGTTVTVSSGSEQKLISEEDLNHHH 300
QY 301 HHKL 304
DB 301 HHKL 304

RESULT 4
AD052296
ID AD052296 standard; protein; 304 AA.
XX AC AD052296;
XX DT 29-JUL-2004 (first entry)
XX DE Human antibody H11 scfv protein #1.
XX KW Antigen binding fragment; H chain V region; L chain V region; C-antigen;
XX KW neoplasia; cancer; vaccine; gene therapy; human;
XX KW single chain V region fragment; scfv.
XX OS Homo sapiens.
XX FH Key
XX FT Misc-difference 302.303
XX FT /note="Encoded by CATTAGTGAAG"
XX PN US2004091484-A1.
XX PD 13-MAY-2004.
XX PF 29-AUG-2003; 2003US-00651453.
XX PR 22-MAY-1996; 96US-00657449.
XX PR 22-MAY-1997; 97US-00862124.
XX PR 13-FEB-2001; 2001US-00782397.
XX PA (DANM/) DAN M D.
XX PA (MATT/) MATTI P K.
XX PA (KAPL/) KAPLAN H A.
XX PA (GRAD/) GRAD C.
XX PI Dan MD, Maiti PK, Kaplan HA, Grad C;
XX PS WPI: 2004-399136/37.
XX PS N-PSDB; AD052295.
XX PT Composition useful for treating neoplasia in patient, comprises antigen
XX PT binding fragment of antibody specifically recognizing C-antigen
XX PT recognized by antibody comprising H chain V region and L chain V region.
XX SS Claim 5; SEQ ID NO 14; 56pp; English.
XX CC The invention relates to a composition comprising an antigen binding
XX CC fragment of an antibody comprising H chain V region and L chain V region
XX CC that specifically recognises C-antigen. The invention is useful for
XX CC treating a patient with a neoplasia. The antigen binding fragment of the
XX CC antibody is used as diagnostic and imaging reagents. The invention is
XX CC useful for genetically altering cells in vivo, to treat various types of
XX CC cancer. It is also useful in vaccine and gene therapy. The present
XX CC sequence is human antibody H11 single chain V region fragment (scfv).

```

SQ Sequence 304 AA;  
 Query Match 100.0%; Score 1582; DB 8; Length 304;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-102;  
 Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC fragments to bind specifically to the C-antigen on cancer cells. Such  
 CC antigen binding fragments may be used for treating a patient with  
 CC neoplasia. It is especially useful in the detection of lymphomas and  
 CC leukemias where the tumor cells bearing the C antigen are circulating  
 CC in the patients bloodstream. The polynucleotide sequence may be used as a  
 CC primer or a probe and the encoded protein may be used in a vaccine or for  
 CC gene therapy. The human monoclonal antibody (Mab), designated H11,  
 CC specifically recognizes cancerous cells. H11 is specific for  
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,  
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and  
 CC prostate adenocarcinoma  
 XX  
 QY 1 EFMKKTALIAVALAGFATVAQADIVLTQSPTLSLSPGERATLSCRAQSQSVSSSYLAWY 60  
 DB 1 EFMKKTALIAVALAGFATVAQADIVLTQSPTLSLSPGERATLSCRAQSQSVSSSYLAWY 60  
 QY 61 QOKPGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDPAVYYCCQYGSFPQ 120  
 DB 61 QOKPGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDPAVYYCCQYGSFPQ 120  
 QY 121 TPQITFGGGTGYEIKRTVAAPSVGGSGGSGGSGGSGGVVQPGRSRLRLS 180  
 DB 121 TPQITFGGGTGYEIKRTVAAPSVGGSGGSGGSGGSGGVVQPGRSRLRLS 180  
 QY 181 CAASGPPRSPFAMHVRQALGKLEWVAVISYDSTKRYAASVKGRFTISRDTSKNTYYL 240  
 DB 181 CAASGPPRSPFAMHVRQALGKLEWVAVISYDSTKRYAASVKGRFTISRDTSKNTYYL 240  
 QY 241 KMSLRTEDTAVYYCARDQSLGDYHYGIDVWGKGTIVVSSGSEOKLISEEDLNHHH 300  
 DB 241 KMSLRTEDTAVYYCARDQSLGDYHYGIDVWGKGTIVVSSGSEOKLISEEDLNHHH 300  
 QY 301 HHKL 304  
 DB 301 HHKL 304  
 RESULT 5  
 AAM40071 standard; protein; 287 AA.  
 XX  
 AC AAM40071;  
 XX  
 DT 29-MAY-1998 (first entry)  
 XX  
 DE Human H11-scFv construct dimer forming protein.  
 XX  
 KM H11; monoclonal antibody; Mab; C-antigen; variable region heavy chain;  
 KM V region; H chain; neoplasia; detection; lymphoma; tumor cell; probe;  
 KM primer; vaccine; gene therapy; glioblastoma; neuroblastoma;  
 KM malignant melanoma; adenocarcinoma; small cell lung carcinoma;  
 KM single chain variable region; scFv.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN MO9744461-A2.  
 XX  
 PD 27-NOV-1997.  
 XX  
 PF 22-MAY-1997; 97MO-US008962.  
 XX  
 PR 22-MAY-1996; 96US-00657449.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Dan MD, Malti PK, Kaplan HA;  
 XX  
 DR WPI; 1998-018515/02.  
 DR N-PSDB; AAV10119.  
 XX  
 PT Antigen binding fragment from monoclonal antibody, H11 - allows tumour  
 PT specific detection and treatment of neoplasia.  
 XX  
 PS Claim 5; Page 95-96; 126pp; English.  
 CC This sequence represents a human H11 monoclonal antibody single chain V  
 CC region fragment (H11-scFv) construct which is capable of forming dimers.  
 CC This construct is used to determine the ability of H11-scFv antibody

CC fragments to bind specifically to the C-antigen on cancer cells. Such  
 CC antigen binding fragments may be used for treating a patient with  
 CC neoplasia. It is especially useful in the detection of lymphomas and  
 CC leukemias where the tumor cells bearing the C antigen are circulating  
 CC in the patients bloodstream. The polynucleotide sequence may be used as a  
 CC primer or a probe and the encoded protein may be used in a vaccine or for  
 CC gene therapy. The human monoclonal antibody (Mab), designated H11,  
 CC specifically recognizes cancerous cells. H11 is specific for  
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,  
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and  
 CC prostate adenocarcinoma  
 XX  
 SQ Sequence 287 AA;  
 Query Match 92.3%; Score 1460.5; DB 2; Length 287;  
 Best Local Similarity 93.8%; Pred. No. 9.7e-94;  
 Matches 285; Conservative 0; Mismatches 2; Indels 17; Gaps 1;  
 CC fragments to bind specifically to the C-antigen on cancer cells. Such  
 CC antigen binding fragments may be used for treating a patient with  
 CC neoplasia. It is especially useful in the detection of lymphomas and  
 CC leukemias where the tumor cells bearing the C antigen are circulating  
 CC in the patients bloodstream. The polynucleotide sequence may be used as a  
 CC primer or a probe and the encoded protein may be used in a vaccine or for  
 CC gene therapy. The human monoclonal antibody (Mab), designated H11,  
 CC specifically recognizes cancerous cells. H11 is specific for  
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,  
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and  
 CC prostate adenocarcinoma  
 XX  
 QY 1 EFMKKTALIAVALAGFATVAQADIVLTQSPTLSLSPGERATLSCRAQSQSVSSSYLAWY 60  
 DB 1 EFMKKTALIAVALAGFATVAQADIVLTQSPTLSLSPGERATLSCRAQSQSVSSSYLAWY 60  
 QY 61 QOKPGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDPAVYYCCQYGSFPQ 120  
 DB 61 QOKPGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDPAVYYCCQYGSFPQ 120  
 QY 121 TPQITFGGGTGYEIKRTVAAPSVGGSGGSGGSGGSGGVVQPGRSRLRLS 180  
 DB 121 TPQITFGGGTGYEIKRTVAAPSVGGSGGSGGSGGSGGVVQPGRSRLRLS 163  
 QY 181 CAASGPPRSPFAMHVRQALGKLEWVAVISYDSTKRYAASVKGRFTISRDTSKNTYYL 240  
 DB 164 CAASGPPRSPFAMHVRQALGKLEWVAVISYDSTKRYAASVKGRFTISRDTSKNTYYL 223  
 QY 241 KMSLRTEDTAVYYCARDQSLGDYHYGIDVWGKGTIVVSSGSEOKLISEEDLNHHH 300  
 DB 224 KMSLRTEDTAVYYCARDQSLGDYHYGIDVWGKGTIVVSSGSEOKLISEEDLNHHH 283  
 QY 301 HHKL 304  
 DB 284 HHKL 287  
 RESULT 6  
 AAE00948 standard; protein; 287 AA.  
 XX  
 AC AAE00948;  
 XX  
 DT 04-JUL-2001 (first entry)  
 XX  
 DE Human monoclonal antibody H11-single chain variable region (scFv) #2.  
 XX  
 KM Human; monoclonal antibody; Mab; H11; single chain variable region; scFv;  
 KM neoplastic disease; melanoma; immunoglobulin IGM; gene therapy; lymphoma;  
 KM carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;  
 KM neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;  
 KM C-antigen; chronic leukaemia; glioma.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key location/Qualifiers  
 FH Misc-difference 285..286  
 FT /note="Encoded by CATTAGTGAAG"  
 FT  
 PN US6207153-B1.  
 XX  
 PD 27-MAR-2001.  
 XX  
 PF 22-MAY-1997; 97US-00862124.  
 XX  
 PR 22-MAY-1996; 96US-00657449.  
 XX

PA (VIVE-) VIVENTIA BIOTECH INC.  
 XX Dan MD, Maiti PK, Kaplan HA;  
 FI  
 XX MPI; 2001-289584/30.  
 DR N-PSDB; AAD04539.  
 XX  
 PT Composition comprising antigen binding fragments of an antibody that  
 PT recognizes an antigen on neoplastic cells but not on normal cells for use  
 PT in diagnosis, imaging and treatment of carcinomas.  
 XX  
 PS Disclosure; Col 69-70; 56pp; English.  
 XX  
 CC The present sequence is human monoclonal antibody (Mab), H11-single chain  
 CC variable region (scFv). The H11 light chain variable region is linked to  
 CC the heavy chain variable region through a (SGGGG)3 linker to form dimers.  
 CC The invention relates to human monoclonal antibody (Mab) H11, H11-(scFv)  
 CC single chain variable (V) region fragment and their corresponding DNA  
 CC molecules. H11 antibody is an immunoglobulin of IGM subclasses which is  
 CC specific to C-antigen found specifically on neoplastic cells and not on  
 CC normal cells. H11 is an antibody obtained from the fusion of peripheral  
 CC blood lymphocytes of a 64 year old male with a low grade glioma and fused  
 CC to a human myeloma cell line to produce a hybridoma designated NBGM1/H11.  
 CC A pharmaceutical composition comprising H11 and its derivatives are  
 CC useful in the diagnosis, imaging and treatment of neoplastic disease,  
 CC particularly, melanoma, breast carcinoma, lung carcinoma, ovarian  
 CC carcinoma, colon carcinoma, gastric carcinoma, prostate carcinoma,  
 CC lymphoma carcinoma, neuroblastoma, glioma, soft tissue sarcoma, small  
 CC cell lung carcinoma, prostatic adenocarcinoma, B and T cell lymphomas and  
 CC chronic leukaemias. H11 DNA is also used in vaccines and gene therapy  
 XX  
 SQ Sequence 287 AA;

Query Match 92.3%; Score 1460.5; DB 4; Length 287;  
 Best Local Similarity 93.8%; Pred. No. 9.7e-94;  
 Matches 285; Conservative 0; Mismatches 2; Indels 17; Gaps 1;

QY 1 EFMKKTAAIAVVALGAFATVAQADIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWY 60  
 DB 1 EFMKKTAAIAVVALGAFATVAQADIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWY 60  
 QY 61 OOKPQAPRLLYGASTRATGMPDRPSSGSGTDFLTLSLEPEDPAFYVCOQYQSSPQ 120  
 DB 61 OOKPQAPRLLYGASTRATGMPDRPSSGSGTDFLTLSLEPEDPAFYVCOQYQSSPQ 120  
 QY 121 TPQITFGGCTKVEIKRTVAAPSVSGGSGGSGGSGGSGQVQLVSGGQVQPGKSLRLS 180  
 DB 121 TPQITFGGCTKVEIKRTVAAPSVSGGSGGSGGSGGSGQVQLVSGGQVQPGKSLRLS 180  
 QY 121 TPQITFGGCTKVEIKRTVAAPSVSGGSGGSGGSGGSGQVQLVSGGQVQPGKSLRLS 163  
 DB 121 TPQITFGGCTKVEIKRTVAAPSVSGGSGGSGGSGGSGQVQLVSGGQVQPGKSLRLS 163  
 QY 161 CAASGPPFRSPAMHWVRQALGKLEWVAIVSYDGTKYVADSVKGRFTISRDTSKNTVYL 240  
 DB 161 CAASGPPFRSPAMHWVRQALGKLEWVAIVSYDGTKYVADSVKGRFTISRDTSKNTVYL 240  
 QY 241 KNSLSRTETATAYVYCARQDQSLGVDHYVGLVWCKTGVTVVSSGSEQLLSEEDLNHHH 300  
 DB 241 KNSLSRTETATAYVYCARQDQSLGVDHYVGLVWCKTGVTVVSSGSEQLLSEEDLNHHH 300  
 QY 301 HHKL 304  
 DB 284 HHKL 287

RESULT 7  
 ID ABU10487 standard; protein; 287 AA.  
 AC ABU10487;  
 DT 07-AUG-2003 (first entry)  
 DE C-antigen antibody H11 single chain variable region fragment #2.  
 KW Human; antibody; H11; single chain variable region; gene therapy; scFv;

KW neoplasia; tumour; recurrence risk; C-antigen; melanoma; neuroblastoma;  
 KW glioma; soft tissue sarcoma; small cell lung carcinoma; brain cancer;  
 KW C-antigen specific antibody; alphac; cancer; vaccine.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Misc-difference 285.286  
 FT /note= "Encoded by CATTAGTAAAG"  
 XX  
 XX US2003021779-A1.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 13-FEB-2001; 2001US-00782397.  
 XX  
 PR 22-MAY-1996; 96US-00657449.  
 PR 22-MAY-1997; 97US-00862124.  
 XX  
 PA (DANM/) DAN M D.  
 PA (MAITI/) MAITI P K.  
 PA (KAPL/) KAPLAN H A.  
 XX  
 PI Dan MD, Maiti PK, Kaplan HA;  
 XX  
 XX MPI; 2003-456278/43.  
 DR N-PSDB; ACA62170, ACA62171.  
 XX  
 PT Novel antigen binding fragment of monoclonal antibody specific for  
 PT antigen detected on neoplastic cells, useful for diagnosing or treating  
 PT cancer, for manufacturing novel reagents and as diagnostic and imaging  
 PT reagent.  
 XX  
 PS Claim 5, Page 36-37; 62pp; English.  
 XX  
 CC The invention relates to a polypeptide which is an antigen binding  
 CC fragment of a monoclonal antibody specific for an antigen detected on  
 CC neoplastic cells. The antigen binding fragment (ABF) is useful for  
 CC treating a patient with a neoplasia. The individual has a clinically  
 CC detectable tumour. The method is useful for palliating the neoplasia. The  
 CC method reduces the risk of recurrence of a clinically detectable tumour.  
 CC The antigen binding fragment is labelled with a therapeutic moiety such  
 CC as radioisotopes or immunomodulators. ABF is useful for detecting C-  
 CC antigen in a sample. The polypeptide is useful for diagnosing, localising  
 CC and/or treating neoplasias, including melanoma, neuroblastoma, glioma,  
 CC soft tissue sarcoma and small cell lung carcinoma. The polypeptide is  
 CC useful for manufacturing novel reagents and for treating and imaging  
 CC brain cancer. ABF is useful as a diagnostic and imaging reagent. The  
 CC composition is useful for eliciting an immune response against neoplasia.  
 CC The polynucleotide is useful in expression systems for the production of  
 CC C-antigen specific antibody, termed H11 or alphac, as hybridisation  
 CC probes to assay for the presence of alphac polynucleotide or related  
 CC sequences in a sample, as primers to effect amplification of desired  
 CC polynucleotides and in pharmaceutical compositions including vaccines and  
 CC for gene therapy. The polynucleotide is also useful for genetically  
 CC altering cells in vivo, thus treating various types of cancer. The  
 CC polypeptide, polynucleotide and the composition are useful for detecting  
 CC or treating cancer, including therapy of cancer and prophylactic care,  
 CC particularly for decreasing the risk of recurrence. The present sequence  
 CC represents the amino acid sequence of the human C-antigen specific  
 CC antibody H11 single chain variable region fragment, scFv, #2  
 XX  
 SQ Sequence 287 AA;

Query Match 92.3%; Score 1460.5; DB 7; Length 287;  
 Best Local Similarity 93.8%; Pred. No. 9.7e-94;  
 Matches 285; Conservative 0; Mismatches 2; Indels 17; Gaps 1;

QY 1 EFMKKTAAIAVVALGAFATVAQADIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWY 60  
 DB 1 EFMKKTAAIAVVALGAFATVAQADIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWY 60



PT protein tyrosine kinase (RPTK) and block constitutive activation of RPTK,  
 CC useful for treating bone and cartilage disorders, or malignant cell  
 PT proliferative diseases.

PS Example 3; Fig 298; 122pp; English.

CC The present invention describes a molecule (1) comprising the antigen  
 CC binding portion of an isolated antibody which has specific binding  
 CC affinity for a receptor protein tyrosine kinase (RPTK), particularly for  
 CC a fibroblast growth factor receptor (FGFR), and which blocks constitutive  
 CC activation of an RPTK. Also described: (1) pharmaceutical compositions  
 CC comprising (1) as an active ingredient and a pharmaceutical carrier,  
 CC excipient, or auxiliary agent; (2) a kit comprising (1), at least one  
 CC reagent for detecting the presence of (1) when bound to the RPTK, and  
 CC instructions for use; (3) a method for treatment of bone and cartilage  
 CC related disorders by administering a composition of (1) to the subject;  
 CC (4) a method for treating or inhibiting a cell proliferative disease or  
 CC disorder by administering the composition of (1); (5) a method for  
 CC screening a molecule comprising the antigen-binding portion of an  
 CC antibody which blocks ligand-dependent activation of RPTK; (6) an  
 CC isolated nucleic acid molecule encoding a V<sub>H</sub>-CDR3 DNA region; (6) an  
 CC CDR3 DNA region; (7) an isolated nucleic acid molecule encoding V<sub>L</sub> region  
 CC and a V<sub>H</sub> region; (8) vectors comprising a nucleic acid molecule of (6) or  
 CC (7); and (9) host cells transformed with the vector. (1) have  
 CC osteopathic, cytostatic and ophthalmological activities, and can be used  
 CC as a RPTK inhibitor. Compositions comprising (1) are useful for treating  
 CC bone and cartilage disorders, including skeletal disorders such as  
 CC skeletal dysplasia (achondroplasia, thanatophoric dysplasia,  
 CC hypochondroplasia, severe achondroplasia with developmental delay and  
 CC acanthosis nigricans dysplasia) or a craniosynostosis disorder (e.g.  
 CC Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis  
 CC nigricans). The composition may also be used for treating or inhibiting  
 CC malignant cell proliferative disease or disorder associated with abnormal  
 CC RPTK activity, including a haematopoietic malignancy (e.g. multiple  
 CC myeloma), solid tumours (e.g. mammary, colon, cervical, bladder,  
 CC colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary  
 CC tumours, tumour progression (particularly progression of transitional  
 CC cell carcinoma or mammary carcinoma), or tumour metastasis, where the  
 CC cell proliferative disorder may be associated with the action of a  
 CC constitutively activated RPTK, or with ligand-dependent activation of  
 CC RPTK. The compositions may further be used for treating  
 CC hyperproliferative diseases and disorders associated with ligand-  
 CC dependent RPTK signaling, such as vision disorders (e.g. neovascular  
 CC glaucoma, macular degeneration and proliferative retinopathy including  
 CC diabetic retinopathy), and non-neoplastic angiogenic pathologic  
 CC conditions (e.g. haemangiomas, angiofibromas and psoriasis). The present  
 CC sequence is given in the exemplification of the present invention.

CC Sequence 638 AA;

Query Match 64.3%; Score 1016.5; DB 6; Length 638;

Best Local Similarity 58.0%; Pred. No. 1.8e-62;

Matches 225; Conservative 15; Mismatches 35; Indels 113; Gaps 5;

QY 3 MKKTAIAIVNAGFTVAQADIVLTQSPGTLISLGERATISCRASQSVSSSYLAWYQO 62  
 DB 1 MKKTAIAIVNAGFTVAQADIVLTQSPATLSLGERATISCRASQSVSSSYLAWYQO 60  
 QY 63 KFGQAPRLIYGASTATGMPDRFSGSGSDPTFTLTISRLEPDPFVYVYCOOVGSSPQRP 122  
 DB 61 KKGQARLLIYGASSTATGVPARFSSGSGSDPTFTLTISRLEPDPFVYVYCOQHYTPP-- 118  
 QY 123 QITFGGTVETIKRTVAAPSV----- 143  
 DB 119 --TFGGTVETIKRTVAAPSVFIPPSDQLKSGTASVCLNNFYPRBAKVQWKVDNAL 176  
 QY 144 -SG-----GGSGGGSGGGG-- 158  
 DB 177 QSGNSQSVTEQDSKDYSLSTLTLSKADYEKKHVAACEVTHQGLSSPVTSSPFRGA 236  
 QY 159 -----SQVQLVESGGGVVQVQPSRSLSCNAGSFPFRSPFAMTWVQ 198  
 DB 237 MKGSTIALALLPLLPVTKAQVQVIVESGGGLVQPGSLRLSCAASGFTFSSYAMSWVQ 296

QY 199 ALGKLEWVAIVSYDSTKYIADSVKGRRTISRDSKNTVYLKMSLRTEDTAVYICAND 258  
 DB 297 APGKLEWVAISLGGSGSTYIADSVKGRFTISRDSKNTLYIQMNSLRADPTAVYICAR- 355  
 QY 259 QSLGDPYHDYGDVWKGKGTIVTSSGS 286  
 DB 356 ----WGGDGFYANDYWGQSTLVVTSAS 379

#### RESULT 10

ADA90139

ID ADA90139 standard; protein; 638 AA.

ADA90139;

20-NOV-2003 (first entry)

Anti-Abeta antibody related amino acid sequence SEQ ID NO:254.

KW antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;  
 KW neurotropic; antiparkinsonian; gene therapy; amyloidogenesis;  
 KW amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia;  
 KW Alzheimer's disease; motor neuropathy; Down's syndrome;  
 KW Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;  
 KW Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;  
 KW neuronal disorder; aging.

OS Synthetic.

PN Homo sapiens.

PN WO2003070760-A2.

PD 28-AUG-2003.

PF 20-FEB-2003; 2003WO-BP001759.

PR 20-FEB-2002; 2002EP-00003844.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PA (MORP-) MORPHOSYS AG.

PI Bardroff M, Bohrmann B, Brockhaus M, Huber W, Kretschmar T;

PI Loehning C, Loetscher H, Nordstedt C, Rothe C;

PI WPI; 2003-663848/62.

PT New antibody molecule capable of specifically recognizing two regions of

PT the beta-A4 peptide, useful for diagnosing, preventing or treating

PT diseases associated with amyloidogenesis or amyloid-plaque formation

PT (e.g. dementia).

PS Disclosure; Page 251-254; 312pp; English.

CC The present invention describes an antibody molecule (1) capable of  
 CC specifically recognizing two regions of the beta-A4 peptide/Abeta4. The  
 CC first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-  
 CC Ser-Gly-Tyr ADA8986 or its fragment, and the second region comprises the  
 CC amino acid sequence Val-His-His-Gln-Lys-Ileu-Val-Phe-Phe-Ala-Glu-Asp-Val-  
 CC Gly ADA8987 or its fragment. Also described: (1) a nucleic acid molecule  
 CC encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host  
 CC cell comprising the vector of (2); (4) preparing (1), comprising  
 CC culturing the host cell of (3) under conditions that allow synthesis of  
 CC (1) and recovering (1) from the culture; (5) a composition comprising (1)  
 CC or an antibody molecule produced by method (4); (6) a kit comprising  
 CC nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising  
 CC (1); (8) testing the resulting Fab optimisation library by panning  
 CC against Abeta4/Abeta4; (9) identifying optimised clones; (10) expressing  
 CC of selected, optimised clones; (11) preparing a pharmaceutical  
 CC composition, comprising optimisation of (1), and formulating the  
 CC optimised antibody/antibody molecule with a carrier; and (12) a  
 CC pharmaceutical composition prepared by method (8). (1) has  
 CC neuroprotective, neurotropic and antiparkinsonian activities, and can be



DB 177 QSGNSQESVTEODSKDSTYSLSSTLTLSKADYEKKHVAACEVTHQGLSPVTKSFNRGEA 236  
 QY 159 -----SQVQLVESGGGVVQVQPSRLRLSCAASGPPRFAMHWQ 198  
 DB 237 MKQSTITALALPLPTPTKAVQVLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWAQ 296  
 QY 199 ALGKLEWVAIVSYDSTKYVADSVKGRFTISRDTSKNTVYKMSLTREDPAVYYCARD 258  
 DB 297 AFGKLEWVAIVSGSGSTYYADSVAGRTTISRDNKNTLYIQMNSLRADPAVYYCAR- 355  
 QY 259 QSLGDDYHYGGLDWGKGTITVSSGS 286  
 DB 356 ----WGDDGFYAMDYWGQGLTVTSSAS 379

RESULT 12  
 ADG74355  
 ID ADG74355 standard; protein; 747 AA.  
 XX  
 AC ADG74355;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE MSPRO light chain variable region protein, SEQ ID NO 92.  
 XX  
 KM antigen binding; receptor protein tyrosine kinase;  
 KM fibroblast growth factor receptor 3; FGFR3; osteoblastic; cytosolic;  
 KM neurotrophic; neuroprotective; ophthalmological; antidiabetic; gene therapy;  
 KM bone; cartilage; cranioynostosis; skeletal dysplasia;  
 KM cell proliferative disorder; haematopoietic malignancy;  
 KM hyperproliferative disorder; neurovascular glaucoma;  
 KM macular degeneration; proliferative retinopathy; diabetic retinopathy;  
 KM MSPRO.  
 KM  
 OS Unidentified.  
 XX  
 PN MO2002102972-A2.  
 XX  
 PD 27-DEC-2002.  
 XX  
 PF 20-JUN-2002; 2002WO-IL000494.  
 XX  
 PR 20-JUN-2001; 2001US-0299187P.  
 XX  
 PA (PROC-) PROCHON BIOTECH LTD.  
 PA (MORP-) MORPHOSYS AG.  
 PI Yajon A, Rom E, Thomassen-Wolf E, Borges E;  
 XX  
 WIPI, 2003-175235/17.  
 XX  
 PT New antigen binding portion of an antibody having a specific binding  
 PT affinity for a receptor protein tyrosine kinase, useful for treating bone  
 PT and cartilage related disorders, cell proliferative or hyperproliferative  
 PT disorders.  
 XX  
 PS Claim 42; SEQ ID NO 92; 122pp; English.  
 XX  
 CC The invention relates to a novel molecule comprising the antigen binding  
 CC portion of an isolated antibody having a specific binding affinity for a  
 CC receptor protein tyrosine kinase, and which blocks constitutive  
 CC activation of a receptor protein tyrosine kinase, such as fibroblast  
 CC growth factor receptor 3 (FGFR3). The novel molecules of the invention  
 CC have the following activities: osteopathic, cytosolic, neurotrophic,  
 CC neuroprotective, ophthalmological, and antidiabetic. The nucleic acids  
 CC encoding the novel molecules of the invention can be used in gene therapy  
 CC to treat disorders. The molecule and nucleic acid molecules are useful  
 CC for treating bone and cartilage related disorders such as  
 CC cranioynostosis (e.g. Muenke coronal cranioynostosis or Crouzon  
 CC syndrome with acanthosis nigricans), or skeletal dysplasia (e.g.  
 CC achondroplasia, thanatophoric dysplasia (TD), hypochondroplasia, severe  
 CC dysplasia), cell proliferative disorders, haematopoietic malignancy (e.g.

CC multiple myeloma), hyperproliferative disorders, neurovascular glaucoma,  
 CC macular degeneration or proliferative retinopathy including diabetic  
 CC retinopathy. This sequence represents an MSPRO antibody light chain  
 CC variable region peptide relating to the invention.  
 XX  
 SQ Sequence 747 AA;  
 QY Query Match 64.3%; Score 1016.5; DB 7; Length 747;  
 DB Best Local Similarity 58.0%; Pred. No. 2.2e-62;  
 DB Matches 225; Conservative 15; Mismatches 35; Indels 113; Gaps 5;  
 QY 3 MKKTAIAVALAGPATVQAQDIIVLTQSPRATLSRGERATLSCRASQSVSSYLAWQ 62  
 DB 110 MKKTAIAVALAGPATVQAQDIIVLTQSPRATLSRGERATLSCRASQSVSSYLAWQ 169  
 QY 63 KPGQAPRLIIYGASTRAATGMPDRFSGSGGTDTFTLTISRLEPEDFAVYYCQOYGSSTP 122  
 DB 170 KPGQAPRLIIYGASTRAATGMPDRFSGSGGTDTFTLTISRLEPEDFAVYYCQOYHTTP 227  
 QY 123 QITFGGQTKVEIKRTVAAPSV----- 143  
 DB 228 --TFGGQTKVEIKRTVAAPSVFIPPPSDQLKSGTASVCLINFPYRAKYQWKVDNAL 285  
 QY 144 -SG-----GGSGGGSGSGG-- 158  
 DB 286 QSGNSQESVTEODSKDSTYSLSSTLTLSKADYEKKHVAACEVTHQGLSPVTKSFNRGEA 345  
 QY 159 -----SQVQLVESGGGVVQVQPSRLRLSCAASGPPRFAMHWQ 198  
 DB 346 MKQSTITALALPLPTPTKAVQVLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWAQ 405  
 QY 199 ALGKLEWVAIVSYDSTKYVADSVKGRFTISRDTSKNTVYKMSLTREDPAVYYCARD 258  
 DB 406 AFGKLEWVAIVSGSGSTYYADSVAGRTTISRDNKNTLYIQMNSLRADPAVYYCAR- 464  
 QY 259 QSLGDDYHYGGLDWGKGTITVSSGS 286  
 DB 465 ----WGDDGFYAMDYWGQGLTVTSSAS 488

RESULT 13  
 AA44994  
 ID AA44994 standard; protein; 523 AA.  
 XX  
 AC AA44994;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE HD706CFV-CH1-GM-CSF chain.  
 XX  
 KM HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EPCAM;  
 KM epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;  
 KM granulocyte/macrophage colony stimulating factor; heteromultimer;  
 KM CHI-domain; multifunctional compound; heavy chain constant domain;  
 KM immunoglobulin; cytosolic; immunostimulatory; anti-leukemia; diagnosis;  
 KM antiproliferative; prevention; treatment; malignant; haematopoietic cell;  
 KM lymphoma; leukaemia; solid tumour; carcinoma; sarcoma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200006605-A2.  
 XX  
 PD 10-FEB-2000.  
 XX  
 PF 28-JUL-1999; 99WO-EP005416.  
 XX  
 PR 28-JUL-1998; 98EP-00114082.  
 XX  
 PA (MICR-) MICROMET GBS BIOMEDIZINISCHE FORSCHUNG.  
 PI Kufer P, Dreier T, Baerle PA, Borchert K, Zettl F;  
 WIPI, 2000-195265/17.

DR N-PSDB; AAZ50587.  
 XX New multifunctional compounds useful for preventing and/or treating  
 PT malignant cell growth and for detection and diagnosis.  
 XX  
 XX Example 10; Fig 55A; 166pp; English.  
 XX  
 CC The patent discloses heteromimibodies which are multifunctional compounds  
 CC producible in a mammalian host cell as a secretable and fully functional  
 CC heterodimer of two polypeptide chains, where one of the polypeptide  
 CC chains comprises, a CH1-domain (constant domain of an immunoglobulin  
 CC heavy chain) and the other chain comprises CL-domain (constant domain of  
 CC an immunoglobulin light chain). The polypeptide chains further comprise,  
 CC fused to the constant domains at least two (poly)peptides having  
 CC different receptor or ligand functions, where further at least two of the  
 CC different (poly)peptides lack an intrinsic affinity for one another and  
 CC are linked via the constant domains. The heteromimibodies have  
 CC cytostatic, immunostimulatory, antileukaemia and antiproliferative  
 CC activities. These compounds can be used for diagnosing, preventing and  
 CC treating malignant cell growth related to malignancies of haematopoietic  
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,  
 CC melanomas and sarcomas. The present sequence is the left chain of a  
 CC heteromimibody comprising HD70 single-chain Fv (scFv) fragment N-  
 CC terminally linked to human CH1 domain which bears at its C-terminus the  
 CC human inflammatory cytokine granulocyte/macrophage colony stimulating  
 CC factor (GM-CSF), plus a hexahistidine sequence for ease of purification.  
 CC HD70 scFv specifically recognises the human epithelial cell adhesion  
 CC molecule (EPCAM) also called 17-1A antigen  
 XX  
 SQ Sequence 523 AA;  
 Query Match 62.3%; Score 986; DB 3; Length 523;  
 Best Local Similarity 69.2%; Pred. No. 1.9e-60;  
 Matches 193; Conservative 32; Mismatches 38; Indels 16; Gaps 4;  
 QY 10 IAVLAGFATVAQADIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAMYQKPGQAPR 69  
 Db 6 ILFLVATATGVHSELQMTQSPSSLSASVGDRTITCRASQSI--SSYLMMWYQKPGQAPR 64  
 QY 70 LLIYGASTRATGMPDRPFGSGSGSTDFLTITSLRLEPEDPAVYVCOYSSPQTPTTFGGG 129  
 Db 65 LLIYMASTRBSGVDPDRFGSGSGSTNTYLTITSLQPEDPAVYVFCQSDSLP---ITFGGG 120  
 QY 130 TKVEIKRTVAAPSVSGGGSGGGSGGSGGVQVLVESGGGVVQPGSRIRLSCAASGPEPR 189  
 Db 121 TRLDIQ-----GGGSGGGSGGGSGGGSEVQLLESGGGVVQPGSRIRLSCAASGPTFS 171  
 QY 190 SPAMHWRAQALGKLEWNAVIVSYDGSITKYVADSVKGRFTISRDTSKNTVYLYKNNSLRTE 249  
 Db 172 SYGMHWRAQAPGKLEWNAVIVSYDGSINKKYADSVKGRFTISRDNSKNTVYLYQNSLRARD 231  
 QY 250 TAVYYCARQDSLLGDYD--HYGLDWGKGTITVSSGS 286  
 Db 232 TAVYYCAKDMGSGMWRPYTYGMDVWGQGITVTVSSGT 270  
 RESULT 14  
 AA444995  
 ID AA444995 standard; protein; 524 AA.  
 XX  
 XX AA444995;  
 DE 23-MAY-2000 (first entry)  
 DT  
 XX  
 XX HD70scFv-Ch-interleukin 2.  
 XX  
 KW HD70; single-chain Fv fragment; scFv; antibody; 17-1A antigen; human;  
 KW EPCAM; epithelial cell adhesion molecule; inflammatory cytokine; IL-2;  
 KW interleukin-2; Ch-domain; constant domain of an immunoglobulin  
 KW heteromimibody; multifunctional compound; immunoglobulin; cytostatic;  
 KW immunostimulatory; antileukaemia; diagnosis; prevention;  
 KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;  
 KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma.

XX OS Homo sapiens.  
 XX PN WO200006605-A2.  
 XX  
 XX 10-FEB-2000.  
 PD  
 XX 28-UTL-1999; 99WO-EP005416.  
 PF  
 XX 28-JUL-1998; 98EP-00114082.  
 PR  
 XX (MICK-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.  
 PA  
 XX Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl P;  
 PT MPI; 2000-195265/17.  
 DR N-PSDB; AAZ50588.  
 XX  
 PT New multifunctional compounds useful for preventing and/or treating  
 PT malignant cell growth and for detection and diagnosis.  
 XX  
 XX Example 10; Fig 55B; 166pp; English.  
 PS  
 XX The patent discloses heteromimibodies which are multifunctional compounds  
 CC producible in a mammalian host cell as a secretable and fully functional  
 CC heterodimer of two polypeptide chains, where one of the polypeptide  
 CC chains comprises, a CH1-domain (constant domain of an immunoglobulin  
 CC heavy chain) and the other chain comprises CL-domain (constant domain of  
 CC an immunoglobulin light chain). The polypeptide chains further comprise,  
 CC fused to the constant domains at least two (poly)peptides having  
 CC different receptor or ligand functions, where further at least two of the  
 CC different (poly)peptides lack an intrinsic affinity for one another and  
 CC are linked via the constant domains. The heteromimibodies have  
 CC cytostatic, immunostimulatory, antileukaemia and antiproliferative  
 CC activities. These compounds can be used for diagnosing, preventing and  
 CC treating malignant cell growth related to malignancies of haematopoietic  
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,  
 CC melanomas and sarcomas. The present sequence is the right chain of a  
 CC heteromimibody comprising HD70 single-chain Fv (scFv) fragment N-  
 CC terminally linked to human Ck domain (constant domain of immunoglobulin-  
 CC kappa light chain) which bears at its C-terminus the human inflammatory  
 CC cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the  
 CC human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen  
 XX  
 SQ Sequence 524 AA;  
 Query Match 62.3%; Score 986; DB 3; Length 524;  
 Best Local Similarity 69.2%; Pred. No. 1.9e-60;  
 Matches 193; Conservative 32; Mismatches 38; Indels 16; Gaps 4;  
 QY 10 IAVLAGFATVAQADIVLTQSPGTLSPGERATLSCRASQSVSSSYLAAMYQKPGQAPR 69  
 Db 6 ILFLVATATGVHSELQMTQSPSSLSASVGDRTITCRASQSI--SSYLMMWYQKPGQAPR 64  
 QY 70 LLIYGASTRATGMPDRPFGSGSGSTDFLTITSLRLEPEDPAVYVCOYSSPQTPTTFGGG 129  
 Db 65 LLIYMASTRBSGVDPDRFGSGSGSTNTYLTITSLQPEDPAVYVFCQSDSLP---ITFGGG 120  
 QY 130 TKVEIKRTVAAPSVSGGGSGGGSGGSGGVQVLVESGGGVVQPGSRIRLSCAASGPEPR 189  
 Db 121 TRLDIQ-----GGGSGGGSGGGSGGGSEVQLLESGGGVVQPGSRIRLSCAASGPTFS 171  
 QY 190 SPAMHWRAQALGKLEWNAVIVSYDGSITKYVADSVKGRFTISRDTSKNTVYLYKNNSLRTE 249  
 Db 172 SYGMHWRAQAPGKLEWNAVIVSYDGSINKKYADSVKGRFTISRDNSKNTVYLYQNSLRARD 231  
 QY 250 TAVYYCARQDSLLGDYD--HYGLDWGKGTITVSSGS 286  
 Db 232 TAVYYCAKDMGSGMWRPYTYGMDVWGQGITVTVSSGT 270  
 RESULT 15  
 ABJ38670



ID ABJ38670 standard; protein; 628 AA.  
 AC ABJ38670;  
 DT 26-JUN-2003 (first entry)  
 DE Fab expression vector protein SEQ ID No 96.  
 XX  
 XX Cytostatic; osteopathic; cerebroprotective; dermatological; enzyme;  
 XX antigen binding; receptor protein tyrosine kinase; skeletal dysplasia;  
 XX constitutive activation; craniosynostosis; cell proliferative disorder;  
 XX achondroplasia; thanatophoric dysplasia; acanthosis nigricans dysplasia;  
 XX hypochondroplasia; severe achondroplasia; transitional cell carcinoma;  
 XX Muenke coronal craniosynostosis; Crouzin syndrome; acanthosis nigricans;  
 XX tumour progression; osteosarcoma; chondrosarcoma; multiple myeloma;  
 XX mammary carcinoma; fibroblast growth factor receptor 3; FGFR3 protein;  
 XX Fab.  
 OS Homo sapiens.  
 XX  
 XX WO2002102854-A2.  
 XX  
 XX PD 27-DEC-2002.  
 XX  
 XX PF 20-JUN-2002; 2002WO-1B003523.  
 XX  
 XX PR 20-JUN-2001; 2001US-0299187P.  
 XX  
 XX PA (MORP-) MORPHOSYS AG.  
 XX PA (PROC-) PROCHON BIOTECH LTD.  
 XX  
 XX PI Thomassen-Wolf E, Borges E, Yayan A, Rom E;  
 XX  
 XX DR WPI; 2003-167489/16.  
 XX  
 XX PT New molecules having the antigen-binding portion of antibodies that block  
 XX PT activation of receptor protein tyrosine kinase, useful for treating or  
 XX PT inhibiting skeletal dysplasias, craniosynostosis or cell proliferative  
 XX PT disorders.  
 XX  
 XX PS Disclosure; Fig 26B; 103pp; English.  
 XX  
 XX CC The invention relates to a novel molecule comprising the antigen binding  
 XX CC portion of an isolated antibody, which has an increased affinity for a  
 XX CC receptor protein tyrosine kinase and which blocks constitutive activation  
 XX CC of the receptor protein tyrosine kinase. The methods and compositions of  
 XX CC the invention are useful for treating or inhibiting a skeletal dysplasia,  
 XX CC craniosynostosis or a cell proliferative disorder. The skeletal dysplasia  
 XX CC is achondroplasia, thanatophoric dysplasia, hypochondroplasia, severe  
 XX CC achondroplasia with developmental delay or acanthosis nigricans  
 XX CC dysplasia. The craniosynostosis disorder is Muenke coronal  
 XX CC craniosynostosis or Crouzin syndrome with acanthosis nigricans. The cell  
 XX CC proliferative disorder is tumour progression that is progression of  
 XX CC transitional cell carcinoma, osteosarcoma, chondrosarcoma, multiple  
 XX CC myeloma or mammary carcinoma. This sequence represents the protein  
 XX CC derived from a Fab expression vector relating to the protein tyrosine  
 XX CC kinase inhibitor of the invention  
 XX  
 XX SQ Sequence 628 AA;

Query Match 61.5%; Score 972.5; DB 6; Length 628;  
 Best Local Similarity 56.9%; Pred. No. 2.1e-59;  
 Matches 215; Conservative 15; Mismatches 35; Indels 113; Gaps 5;

QY 13 ALAGFATVQADIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLI 72  
 DB 1 ALAGFATVQADIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLI 60  
 QY 73 YASTRATGMPDRPSGSGSGDTFTLTISLPEPDFAVYVCCQYSGSPQRTITFGGTRV 132  
 DB 61 YGASSRATGVPARFSGSGSGDTFTLTISLPEPDFAVYVCCQHYTTP---TFGGTRV 116  
 QY 133 EIKRTVAAPSV-----SG----- 145

DB 117 EIKRTVAAPSVFIPPPSDEQLKSGTASVYCLINNFYPREAKYQMKVDNALQSGNSQESVT 176  
 QY 146 -----GGSGGGGGGGGG----- 158  
 DB 177 EGDSDSTYSLSSTLTLSKADYKHKYVACEVTHQGLSPVTKSFNRGEMKQSTIALAL 236  
 QY 159 -----SOVLVESGGGVVQPGSRSLRLSCAASGFPFRSFAMHWYRQALGKLEWVA 208  
 DB 237 LPDLFTPTVTKAQVQVLESGGGLVQPGSLRLSCAASGFTFSYVAMSWYQADPKGLEWVS 296  
 QY 209 VTSYGSTKYVADSVKGRFTISRDPSKNTVYLNMSLRREDPAVYVCCARDQSLLEDYDH 268  
 DB 297 AISGSGSTYVADSVKGRFTISRDNSKNTLYLNMSLRADDTAVYYCAR-----WGDDGF 351  
 QY 269 YGLDVGKGTITVYVSSGS 286  
 DB 352 YAMDYWGQGITLVYVSSAS 369

Search completed: February 18, 2005, 08:56:01  
 Job time : 84 secs

**THIS PAGE BLANK (usPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2005, 08:47:49 ; Search time 25 Seconds  
(without alignments)  
907.733 Million cell updates/sec

Title: US-09-194-164-14

Perfect score: 1582  
Sequence: 1 EFMKKTATAIAVALAGPATV.....GSEOKLISEEDLNHHHKL 304

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/1/1aa/PCUTS\_COMB.pep:\*
- 6: /cgn2\_6/prodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1582	100.0	304	3	US-08-862-124-14 Sequence 14, Appl
2	1460.5	92.3	287	3	US-08-862-124-17 Sequence 17, Appl
3	928	58.7	352	4	US-09-203-958A-2 Sequence 2, Appl
4	926.5	58.6	456	4	US-09-495-880A-11 Sequence 11, Appl
5	892	56.4	283	4	US-09-420-592A-6 Sequence 6, Appl
6	892	56.4	283	4	US-09-985-442-6 Sequence 6, Appl
7	892	56.4	283	4	US-09-983-580-6 Sequence 6, Appl
8	887	56.1	263	4	US-09-069-821-3 Sequence 3, Appl
9	887	56.1	263	4	US-09-956-086-3 Sequence 3, Appl
10	887	56.1	263	4	US-09-956-087-3 Sequence 3, Appl
11	865	54.7	354	4	US-09-393-627B-28 Sequence 28, Appl
12	827.5	52.3	240	1	US-08-488-113B-147 Sequence 147, App
13	827.5	52.3	240	1	US-08-477-484B-147 Sequence 147, App
14	827.5	52.3	240	2	US-08-646-360-147 Sequence 147, App
15	827.5	52.3	240	3	US-08-839-765-147 Sequence 147, App
16	827.5	52.3	240	3	US-09-136-389-147 Sequence 147, App
17	827.5	52.3	240	4	US-09-610-838-147 Sequence 147, App
18	827.5	52.3	240	4	US-09-711-485-147 Sequence 147, App
19	808.5	51.1	409	4	US-09-554-765-14 Sequence 14, Appl
20	805	50.9	408	4	US-09-554-765-15 Sequence 15, Appl
21	784	49.6	371	2	US-08-400-115-4 Sequence 4, Appl
22	784	49.6	374	4	US-09-646-028-15 Sequence 15, Appl
23	779.5	49.3	491	4	US-10-011-125A-2 Sequence 2, Appl
24	777	49.1	599	1	US-08-442-542-18 Sequence 18, Appl
25	777	49.1	599	3	US-08-765-469-18 Sequence 18, Appl
26	766	48.4	298	3	US-09-318-661-2 Sequence 2, Appl
27	766	48.4	298	4	US-09-883-758-2 Sequence 2, Appl

28	756	47.8	244	2	US-08-392-338A-13 Sequence 13, Appl
29	756	47.8	244	3	US-09-166-750-13 Sequence 13, Appl
30	756	47.8	244	3	US-09-166-093-13 Sequence 13, Appl
31	756	47.8	244	3	US-09-172-019-13 Sequence 13, Appl
32	756	47.8	244	3	US-09-166-094-13 Sequence 13, Appl
33	756	47.8	244	4	US-09-443-213-13 Sequence 13, Appl
34	755	47.7	239	2	US-08-860-174A-2 Sequence 2, Appl
35	744	47.0	242	2	US-08-324-591-14 Sequence 14, Appl
36	744	47.0	242	2	US-08-926-789-14 Sequence 14, Appl
37	744	47.0	242	2	US-08-392-338A-23 Sequence 23, Appl
38	744	47.0	242	3	US-09-166-750-23 Sequence 23, Appl
39	744	47.0	242	3	US-09-166-093-23 Sequence 23, Appl
40	744	47.0	242	3	US-09-172-019-23 Sequence 23, Appl
41	744	47.0	242	3	US-09-166-094-23 Sequence 23, Appl
42	744	47.0	242	4	US-09-443-213-23 Sequence 23, Appl
43	744	47.0	244	5	PCT-US93-11138-14 Sequence 14, Appl
44	744	47.0	285	3	US-09-318-661-4 Sequence 4, Appl
45	744	47.0	285	4	US-09-883-758-4 Sequence 4, Appl

#### ALIGNMENTS

RESULT 1  
US-08-862-124-14  
Sequence 14, Application US/08862124  
Patent No. 6207153  
GENERAL INFORMATION:  
APPLICANT: Dan, Michael D.  
APPLICANT: Maht, Pradipt K.  
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND TREATMENT OF CANCERS  
TITLE OF INVENTION: DETECTION OF CANCERS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/862,124  
FILING DATE: 22-MAY-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 31608-20001.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 304 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-862-124-14  
Query Match 100.0%; Score 1582; DB 3; Length 304;  
Best Local Similarity 100.0%; Pred. No. 2.7e-113;  
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EFMKKTATAIAVALAGPATVADIVLTOSPTLSLSPERATLSCRASQSVSSSTLAWY 60

```
Db 1 EFMKTAIAIIVALAGFATVAQADIVLTQSPTLSLSPGERATLSCRASQSVSSSYLAWY 60
Qy 61 QOKFGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCOQYGSPPQ 120
Db 61 QOKFGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCOQYGSPPQ 120
Qy 121 TPQITFGGKTVEIKRTVAAPSVSGSGSGSGSGSQVQLVSGGTVVQPGSLRLS 180
Db 121 TPQITFGGKTVEIKRTVAAPSVSGSGSGSGSQVQLVSGGTVVQPGSLRLS 180
Qy 181 CAASGPFPRFAMHWRAQALGKLEWAVISYDSTKTYADSVKGRFTISRDTSKNTVYL 240
Db 181 CAASGPFPRFAMHWRAQALGKLEWAVISYDSTKTYADSVKGRFTISRDTSKNTVYL 240
Qy 241 KMSLRTEPTAVYYCARDQSLGIDYHYGLDVGKGTIVTVSSGSBQKLISEEDLNHHH 300
Db 241 KMSLRTEPTAVYYCARDQSLGIDYHYGLDVGKGTIVTVSSGSBQKLISEEDLNHHH 300
Qy 301 HHKL 304
Db 301 HHKL 304
```

```
RESULT 2
US-08-862-124-17
; Sequence 17, Application US/08862124
; Patent No. 6207153
```

```
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
APPLICANT: Maiti, Pradip K.
APPLICANT: Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
NUMBER OF INVENTION: DETECTION OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lehnardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-862-124-17
```

```
Query Match 92.3%; Score 1460.5; DB 3; Length 287;
Best Local Similarity 93.8%; Pred. No. 4.7e-104;
Matches 285; Conservative 0; Mismatches 2; Indels 17; Gaps 1;
```

```
Qy 1 EFMKTAIAIIVALAGFATVAQADIVLTQSPTLSLSPGERATLSCRASQSVSSSYLAWY 60
Db 1 EFMKTAIAIIVALAGFATVAQADIVLTQSPTLSLSPGERATLSCRASQSVSSSYLAWY 60
Qy 61 QOKFGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCOQYGSPPQ 120
Db 61 QOKFGQAPRLIIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCOQYGSPPQ 120
Qy 121 TPQITFGGKTVEIKRTVAAPSVSGSGSGSGSQVQLVSGGTVVQPGSLRLS 180
Db 121 TPQITFGGKTVEIKRTVAAPSVSGSGSGSGSQVQLVSGGTVVQPGSLRLS 180
Qy 181 CAASGPFPRFAMHWRAQALGKLEWAVISYDSTKTYADSVKGRFTISRDTSKNTVYL 240
Db 181 CAASGPFPRFAMHWRAQALGKLEWAVISYDSTKTYADSVKGRFTISRDTSKNTVYL 240
Qy 241 KMSLRTEPTAVYYCARDQSLGIDYHYGLDVGKGTIVTVSSGSBQKLISEEDLNHHH 300
Db 241 KMSLRTEPTAVYYCARDQSLGIDYHYGLDVGKGTIVTVSSGSBQKLISEEDLNHHH 300
Qy 301 HHKL 304
Db 301 HHKL 287
```

```
RESULT 3
US-09-203-958A-2
; Sequence 2, Application US/09203958A
; Patent No. 6682928
```

```
GENERAL INFORMATION:
APPLICANT: KELLER, Tibor
APPLICANT: GOLDSTEIN, Joel
APPLICANT: GRAZIANO, Robert
APPLICANT: DEO, Yashwant M.
TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR
TITLE OF INVENTION: BINDING COMPONENTS
FILE REFERENCE: MXI-099CPA
CURRENT APPLICATION NUMBER: US/09/203,958A
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 60/067232
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-09-203-958A-2
```

```
Query Match 58.7%; Score 928; DB 4; Length 352;
Best Local Similarity 66.4%; Pred. No. 2.8e-63;
Matches 192; Conservative 26; Mismatches 45; Indels 26; Gaps 5;
```

```
Qy 18 ATVAQADIVLTQSPTLSLSPGERATLSCRASQSVSSSYLAWYQOKFGQAPRLII 72
Db 32 AOPASDIQLTQSSLSASVGDVITCKSSQSVLYSSNQKTLAWYQOKFGQAPRLII 91
Qy 73 YGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCOQYGSPPQTPQITFGGKT 132
Db 92 YMASTRSGVPSRSGSGSGTDFTLTISRLEPEDFAVYYCHQYLLS-----WTFGQGT 146
Qy 133 EIKRTVAAPSVSGSGSGSGSQVQLVSGGTVVQPGSLRLSCAASGPFPRSF 192
Db 147 EIKS-----SGGSGSGSGSGSQVQLVSGGTVVQPGSLRLSCSSGFTFSDNY 199
Qy 193 MHWRAQALGKLEWAVISYDSTKTYADSVKGRFTISRDTSKNTVYLKMSLRTEPTAV 252
Db 200 MHWRAQALGKLEWAVISYDSTKTYADSVKGRFTISRDTSKNTVYLFLQNDLSRPE 259
Qy 253 YICARDQSLGIDYHYGLDVGKGTIVTVSSG-----SEQKLISEEDLN 297
```

DB 260 YFCAR-----GYRYEGANDYWGQGTPTVSSPRLQVDEQKLISEBDLN 303

## RESULT 4

US-09-495-880A-11  
Sequence 11, Application US/09495880A

GENERAL INFORMATION:  
APPLICANT: RUDERT, FRITZ  
APPLICANT: GE, LIMING  
APPLICANT: ILAG, VIC  
TITLE OF INVENTION: NOVEL METHOD AND PHAGE FOR THE IDENTIFICATION OF  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIC  
TITLE OF INVENTION: (POLY) PEPTIDE COMPLEX  
FILE REFERENCE: MORPHO/9  
CURRENT APPLICATION NUMBER: US/09/495,880A  
CURRENT FILING DATE: 2000-02-01  
PRIOR APPLICATION NUMBER: PCT/EP98/04836  
PRIOR FILING DATE: 1998-08-03  
PRIOR APPLICATION NUMBER: EP 97 11 3319.4  
PRIOR FILING DATE: 1997-08-01  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 456  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: ompA-FLAG-scFv (anti-  
OTHER INFORMATION: HAg)-gene IIIs encoded by phage vector fHag1A (circular)  
US-09-495-880A-11

Query Match 58.6%; Score 926.5; DB 4; Length 456;

Best Local Similarity 63.1%; Pred. No. 4.9e-63;  
Matches 190; Conservative 37; Mismatches 49; Indels 25; Gaps 6;

QY 3 MKKTAIAVALAGFATVQA---DIVLTQSPGTTSLSPGERATLSCRAQSIVSS---- 55  
DB 1 MKKTAIAVALAGFATVQAQADYKDIWMTQSPSSLTIVTGEVYVMTSCISSQSLFNSGKQK 60  
QY 56 -YLAWYQKPGQAPRLIYGASTRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQO 114  
DB 61 NLTLYQKPGQAPRLIYMASTRSGVDRFTGSGSGSGTDFTLTISRLEPEDFAVYYCQO 120  
QY 115 YGSSPQRTQITFGGTTKVEIKRTVAAP-----VSGGSGSGSGSGSGSGSQVQLVES 166  
DB 121 DYSNP-----LTFGGGTGLEKLRAGGGGSGGSGSGSGSGSGSGSGSGSGSGSGSG 176  
QY 167 GGGVQVQPGSRSLSCAASGFFPRSPAMHWYRQALGKLEWAVIISYDGTSTKYAASVYKGR 226  
DB 177 GGDVLPQGSRLSLSCAASGFFSPSSYGMWVRQTTPDKLEWAVIISNGGTYTPDPSSVYKGR 236  
QY 227 FTISRDTSKNTVYLYKNSLTREDTAVVYICARDQSLGPDHYHGGTLDVWGKGTITVYSSGS 286  
DB 227 FTISDNKNTIYLYQMSLSKSDSAMYCARER-----YDE-NGRAYMGQGLIVTVSASG 291  
QY 287 E 287  
DB 292 E 292

RESULT 5  
US-09-420-592A-6

Sequence 6, Application US/09420592A

GENERAL INFORMATION:  
APPLICANT: Filpula, David R.  
APPLICANT: Wang, Maoliang  
APPLICANT: Whitlow, Marc D.  
TITLE OF INVENTION: No. 6333396e1 Method for Targeted Delivery of Nucleic Acids  
FILE REFERENCE: 0977.2300001  
CURRENT APPLICATION NUMBER: US/09/420,592A  
CURRENT FILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/104,949

PRIOR FILING DATE: 1998-10-20  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 283  
TYPE: PRT

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Kabat  
OTHER INFORMATION: Consensus  
NAME/KEY: UNSURE  
LOCATION: (232)  
OTHER INFORMATION: May be any amino acid.  
NAME/KEY: UNSURE  
LOCATION: (234)  
OTHER INFORMATION: May be any amino acid.  
NAME/KEY: UNSURE  
LOCATION: (239)  
OTHER INFORMATION: May be any amino acid.  
US-09-420-592A-6

Query Match 56.4%; Score 892; DB 3; Length 283;

Best Local Similarity 66.3%; Pred. No. 1.2e-60;  
Matches 181; Conservative 29; Mismatches 47; Indels 16; Gaps 5;

QY 24 DIVLTQSPGTTSLSPGERATLSCRAQSV--SSYLYAWYQKPGQAPRLIYGASTRATG 81  
DB 1 DIQMTQSPSSLSASVGDRVTTCRAQSVLSISNLYAWYQKPGQAPRLIYAASLSLSG 60  
QY 82 MDRFRSGSGSGTDFTLTISRLEPEDFAVYYCQVQSSPQRTQITFGGTTKVEIKRTVAAP 141  
DB 61 VPSRFGSGSGSGTDFTLTISRLEPEDFAVYYCQVNS--LPEWTGQGTKEIKGK----- 113  
QY 142 SVSGGSGSGSGSGSGSQVQLVESGGGVQPGSRSLRLSCAASGFFPRSPAMHWYRQALG 201  
DB 114 --TSGSGKPGQSEGSTKGEVQLVESGGGLVQGGSLRLSCAASGFTFSSAAMSWVRQARG 171  
QY 202 KLEWAVIIS--YDGTSTKYADSVKGRFTISRDTSKNTVYLYKNSLTREDTAVVYICARDQ 259  
DB 172 KLEWAVSYISGKTDGSGTYADSVKGRFTISRDNKNTIYLYQMSLSRLEDTAVVYICARGR 231  
QY 260 ---SLGPDHYHGGTLDVWGKGTITVYSSGSEK 289  
DB 232 XGXSLSGXYHYHYPDWGQGTITVYSSKRRK 264

## RESULT 6

US-09-985-442-6  
Sequence 6, Application US/09985442

PATENT NO. 6692942  
GENERAL INFORMATION:  
APPLICANT: Filpula, David R.  
APPLICANT: Wang, Maoliang  
APPLICANT: Whitlow, Marc D.  
TITLE OF INVENTION: No. 6692942e1 Method for Targeted Delivery of Nucleic Acids  
FILE REFERENCE: 0977.2300003  
CURRENT APPLICATION NUMBER: US/09/985,442  
CURRENT FILING DATE: 2001-11-02  
PRIOR APPLICATION NUMBER: 09/420,592  
PRIOR FILING DATE: 1998-10-19  
PRIOR APPLICATION NUMBER: 60/104,949  
PRIOR FILING DATE: 1998-10-20  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 283  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Kabat  
OTHER INFORMATION: Consensus  
NAME/KEY: UNSURE





APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH U.  
REGISTRATION NUMBER: 40,679  
REFERENCE/DOCKET NUMBER: 0977.2280003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-956-087-3

Query Match 56.1%; Score 887; DB 4; Length 263;  
Best Local Similarity 67.2%; Pred. No. 2,7e-60;  
Matches 180; Conservative 27; Mismatches 45; Indels 16; Gaps 5;

QY 24 DIVLTQSPGTLSPGSRATLSCRASQSV--SSSYLAHQKPGQAPRLIYGASTRATG 81  
DB 1 DIQMTQSPSSLSLTVAAGEKVTMSCKSSQSLNSGNQKYLITVYQKPGQAPRLIYMAST 60  
QY 82 MPDRFSGSGSGSTDTFTLTISRLEPEDPAVYVCOYGSSPQTPOITFGGKTKVEIKRTVAAP 141  
DB 61 VSRKSGSGSGSTDTFTLTISRLEPEDPAVYVCOYNS--LPEWTFGGKTKVEIKRS---- 113  
QY 142 SVSGGGSGSGSGSGGSGGVQVLESQGVVOPGRSLRLSCAASGPFPSFAMHWYRQALG 201  
DB 114 --TSGSGKRGSGSGSGSGGVQVLESQGVVOPGRSLRLSCAASGPFPSFAMHWYRQALG 171  
QY 202 KLEWNAVVIS--YDSTKRYADSVKGRFTISRDTSKNTVYLNKNLSRTEDTAVYYCARQ 259  
DB 172 KLEWNAVVISGKTDGSTYVADSVKGRFTISRDNSKNTVYLNKNLSRAEDTAVYYCARGR 231  
QY 260 ---SLGADYDHYGLDVGWKGKTTVTVSS 284  
DB 232 XGSLSGKXYHYHYFDYWGCGTLVTVSS 259

RESULT 11  
US-09-393-627B-28  
Sequence 28, Application US/09393627B  
Patent No. 6455314

GENERAL INFORMATION:  
APPLICANT: Wickham, Thomas J.  
APPLICANT: Kovesdi, Imre  
APPLICANT: Roelivink, Petrus W.  
APPLICANT: Bruder, Joseph T.  
TITLE OF INVENTION: Alternatively Targeted Adenovirus  
FILE REFERENCE: 202345  
CURRENT APPLICATION NUMBER: US/09/393,627B  
CURRENT FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US 60/099,851  
PRIOR FILING DATE: 1998-09-11  
PRIOR APPLICATION NUMBER: US 60/136,529  
PRIOR FILING DATE: 1999-05-28  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.2  
SEQ ID NO 28  
LENGTH: 354  
TYPE: PRT  
ORGANISM: Anti-HA ScFv fused in frame with 2 C-terminal myc epitopes and PDGF receptor transmembrane anchor (Anti-HA pseudo-receptor)  
US-09-393-627B-28

Query Match 54.7%; Score 865; DB 4; Length 354;

Best Local Similarity 61.2%; Pred. No. 1.8e-58;  
Matches 172; Conservative 42; Mismatches 45; Indels 22; Gaps 6;  
QY 23 ADIVLTQSPGTLSPGSRATLSCRASQSVSSS-----YLAHQKPGQAPRLIYGAST 77  
DB 26 ADIVLTQSPSSLSLTVAAGEKVTMSCKSSQSLNSGNQKYLITVYQKPGQAPRLIYMAST 85  
QY 78 RATGMPDRFSGSGSGSTDTFTLTISRLEPEDPAVYVCOYGSSPQTPOITFGGKTKVEIKRT 137  
DB 86 RSGVDPDRFTGSGSGSGSTDTFTLTISRLEPEDPAVYVCOYNSHP---LTFGAGTKLELR- 140  
QY 138 VAAPSVSGSGSGSGSGSGSGGVQVLESQGVVOPGRSLRLSCAASGPFPSFAMHWYR 197  
DB 141 -----AGGSGSGSGSGSGSGGVQVLESQGVVOPGRSLRLSCAASGPFPSFAMHWYR 194  
QY 188 QALGKLEWNAVVISYDSTKRYADSVKGRFTISRDTSKNTVYLNKNLSRTEDTAVYYCAR 257  
DB 195 QTPNKRLEWVPTLIRGGSYTVYVPSVKGRFTISKNAKNTVYLNKNLSKSEDTAVYYCAK 254  
QY 258 DQSLGADYDHYGLDVGWKGKTTVTVS--SGSEKLISEEDLN 297  
DB 255 RET---FDE-KGFAYWGCGTLVTVSAAAEKLISEEDLN 290

RESULT 12  
US-08-488-113B-147  
Sequence 147, Application US/08488113B  
Patent No. 5744580  
GENERAL INFORMATION:  
APPLICANT: Belter, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 110220US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155



TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 147:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 amino acids  
TYPE: amino acid  
TOPOLOGY: 1 linear  
MOLECULE TYPE: protein  
US-08-488-113B-147

Query Match 52.3%; Score 827.5; DB 1; Length 240;  
Best Local Similarity 61.7%; Pred. No. 8.5e-56;  
Matches 161; Conservative 37; Mismatches 42; Indels 21; Gaps 5;

QY 24 DIVLQSPGCTLSLSPGERATLSCRASQSSSYLAWYQKPGQAPRLIYGASTATGMP 83  
DB 1 DIQWQSPBSLASVQDRVTITCRASQDI-NSYLSWFOQPKAPKTLIYRANRLSGVP 59  
QY 84 DRFGSGSGTDFTLTISRLEPEDFAVYVCOQYSSPQTPIFGGKTKEIKRTVAAPSV 143  
DB 60 SRFSSGSGTDYTLTISSLYQEDFGIYCOQYDESPW----TFGGTKLEMK----- 107  
QY 144 SGGGSGGGGSGGGGSGGVQVLVESGGGVVQPGRLSLRSCAAGFPFRSFMHWVROALGKG 203  
DB 108 -GGGSGGGGSGGGGSGGSEIQLVQSGGLVPGGSVRIISCAASGYTFNTYGMNVVROALPGKG 166  
QY 204 LEWVAVISYDSTKXYADSVKGRFTISRDTSKNTVYLKNSLRTEPTAVYYCARDQSLIG 263  
DB 167 LEWKMVINTHTGEPTVADSFKGRFTFSLDSSKNTAVLQINSRAEDTAVYFCTR-----R 221  
QY 264 DYDHYGLDVWKGKTTVTYSS 284  
DB 222 GYDWF--DVWGGGTTVTYSS 240

RESULT 13  
US-08-477-484B-147  
Sequence 147, Application US/08477484B  
Patent No. 5756699  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,484B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/968,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 147:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 amino acids  
TYPE: amino acid  
TOPOLOGY: 1 linear  
MOLECULE TYPE: protein  
US-08-477-484B-147

Query Match 52.3%; Score 827.5; DB 1; Length 240;  
Best Local Similarity 61.7%; Pred. No. 8.5e-56;  
Matches 161; Conservative 37; Mismatches 42; Indels 21; Gaps 5;

QY 24 DIVLQSPGCTLSLSPGERATLSCRASQSSSYLAWYQKPGQAPRLIYGASTATGMP 83  
DB 1 DIQWQSPBSLASVQDRVTITCRASQDI-NSYLSWFOQPKAPKTLIYRANRLSGVP 59  
QY 84 DRFGSGSGTDFTLTISRLEPEDFAVYVCOQYSSPQTPIFGGKTKEIKRTVAAPSV 143  
DB 60 SRFSSGSGTDYTLTISSLYQEDFGIYCOQYDESPW----TFGGTKLEMK----- 107  
QY 144 SGGGSGGGGSGGGGSGGVQVLVESGGGVVQPGRLSLRSCAAGFPFRSFMHWVROALGKG 203  
DB 108 -GGGSGGGGSGGGGSGGSEIQLVQSGGLVPGGSVRIISCAASGYTFNTYGMNVVROALPGKG 166  
QY 204 LEWVAVISYDSTKXYADSVKGRFTISRDTSKNTVYLKNSLRTEPTAVYYCARDQSLIG 263  
DB 167 LEWKMVINTHTGEPTVADSFKGRFTFSLDSSKNTAVLQINSRAEDTAVYFCTR-----R 221  
QY 264 DYDHYGLDVWKGKTTVTYSS 284  
DB 222 GYDWF--DVWGGGTTVTYSS 240

RESULT 14  
US-08-646-360-147  
Sequence 147, Application US/08646360  
Patent No. 5837491  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05348



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: February 18, 2005, 08:54:45 ; Search time 73 Seconds

(without alignments)  
1362.757 Million cell updates/sec

Title: US-09-194-164-14

Perfect score: 1582  
Sequence: 1 EFMKKTALATVALAGPATV.....GSEQKLISEEDLNHHHKKL 304

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1582	100.0	304	10	US-09-782-397-14 Sequence 14, Appl
2	1582	100.0	304	15	US-10-651-453-14 Sequence 14, Appl
3	1460.5	92.3	287	10	US-09-782-397-17 Sequence 17, Appl
4	1460.5	92.3	287	15	US-10-651-453-17 Sequence 17, Appl
5	928	58.7	352	10	US-09-203-958A-2 Sequence 2, Appl
6	928.5	58.6	456	15	US-10-634-862-11 Sequence 11, Appl
7	892	56.4	283	9	US-09-983-580-6 Sequence 6, Appl
8	892	56.4	283	9	US-09-985-442-6 Sequence 6, Appl
9	887	56.1	263	9	US-09-956-086-3 Sequence 3, Appl
10	887	56.1	263	9	US-09-956-087-3 Sequence 3, Appl
11	866.5	54.8	630	15	US-10-422-628-48 Sequence 48, Appl
12	866.5	54.8	639	15	US-10-422-628-16 Sequence 16, Appl
13	865.5	54.6	277	15	US-10-422-628-43 Sequence 43, Appl

14	857.5	54.2	279	15	US-10-409-938-21	Sequence 21, Appl
15	849.5	53.7	252	15	US-10-423-847-10	Sequence 10, Appl
16	849.5	53.7	253	15	US-10-423-847-14	Sequence 14, Appl
17	849.5	53.7	253	15	US-10-423-847-11	Sequence 11, Appl
18	849.5	53.7	254	15	US-10-423-847-17	Sequence 17, Appl
19	847	53.5	239	15	US-10-423-847-18	Sequence 18, Appl
20	827.5	52.3	240	15	US-10-127-890-147	Sequence 147, App
21	824.5	52.1	247	15	US-10-423-847-13	Sequence 13, Appl
22	824	52.1	443	13	US-10-006-773-2	Sequence 2, Appl
23	824	52.1	443	13	US-10-006-771A-2	Sequence 2, Appl
24	810	51.2	4852	15	US-10-412-406-33	Sequence 33, Appl
25	808.5	51.1	409	15	US-10-353-721-14	Sequence 14, Appl
26	807.5	51.0	502	16	US-10-679-620-88	Sequence 88, Appl
27	806.5	51.0	663	15	US-10-412-406-32	Sequence 32, Appl
28	805	50.9	408	15	US-10-353-721-15	Sequence 15, Appl
29	803.5	50.8	252	9	US-09-971-543-1	Sequence 1, Appl
30	784.5	49.6	364	16	US-10-829-388-11	Sequence 11, Appl
31	784.5	49.6	370	16	US-10-829-388-1	Sequence 1, Appl
32	784	49.6	271	10	US-09-226-157-4	Sequence 4, Appl
33	784	49.6	374	14	US-10-335-394-15	Sequence 15, Appl
34	779.5	49.3	491	13	US-10-011-125-2	Sequence 2, Appl
35	770	48.7	256	15	US-10-418-182-2	Sequence 2, Appl
36	769	48.6	492	14	US-10-207-655-344	Sequence 344, App
37	767.5	48.5	543	14	US-10-207-655-346	Sequence 346, App
38	767	48.5	298	9	US-10-207-655-345	Sequence 345, App
39	766	48.4	543	14	US-09-883-758-2	Sequence 2, Appl
40	766	48.4	536	14	US-10-207-655-268	Sequence 268, App
41	762.5	48.2	431	14	US-10-013-173-4	Sequence 4, Appl
42	762.5	48.2	431	14	US-10-150-762-4	Sequence 4, Appl
43	762.5	48.2	431	14	US-10-244-821-4	Sequence 4, Appl
44	761	48.1	258	14	US-10-207-655-343	Sequence 343, App
45	759.5	48.0	271	14	US-10-207-655-254	Sequence 254, App

## ALIGNMENTS

RESULT 1  
US-09-782-397-14  
; Sequence 14, Application US/09782397  
; Publication No. US20030021799A1  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; ; Maltl, Pradip K.  
; ; Kaplan, Howard A.  
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT  
; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE  
; FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND  
; DETECTION OF CANCERS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster LLP  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/782,397  
; FILING DATE: 13-Feb-2001  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/862,124  
; FILING DATE: 1997-05-22  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lehnardt, Susan K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 31608-20001.20

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-782-397-14

Query Match      100.0%; Score 1582; DB 10; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.8e-95;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFMKKTATAIAVALAGFATVAADIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAMY 60
DB 1 EFMKKTATAIAVALAGFATVAADIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAMY 60
QY 61 OQPGQAPRLILYGASTATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYQSSSPQ 120
DB 61 OQPGQAPRLILYGASTATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYQSSSPQ 120
QY 121 TPQITFGGGTKVEIKRTVAAPSVSGSGSGSGSQVQLVPSGGSVVPQGRSLRLIS 180
DB 121 TPQITFGGGTKVEIKRTVAAPSVSGSGSGSGSQVQLVPSGGSVVPQGRSLRLIS 180
QY 181 CAASGPPRSPFAMHWVRQALGKLEWNAVISTDSTKYAASVKGRFTISRDTSKNTVYL 240
DB 181 CAASGPPRSPFAMHWVRQALGKLEWNAVISTDSTKYAASVKGRFTISRDTSKNTVYL 240
QY 241 KNSLRTEDTAVYYCARQDSLLGDYDHYGLDVGWKGITTVYSSGSEQKLISEEDLNHHH 300
DB 241 KNSLRTEDTAVYYCARQDSLLGDYDHYGLDVGWKGITTVYSSGSEQKLISEEDLNHHH 300
QY 301 HKKL 304
DB 301 HKKL 304

RESULT 2
US-10-651-453-14
; Sequence 14, Application US/10651453
; Publication No. US20040091484A1
; GENERAL INFORMATION:
; APPLICANT: Maici, Michael D.
; APPLICANT: Dan, Michael P.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS,
; TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PRO
; FILE REFERENCE: 316082000103
; CURRENT APPLICATION NUMBER: US/10/651,453
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 09/782,397
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 08/862,124
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: US 08/657,449
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-651-453-14

Query Match      100.0%; Score 1582; DB 15; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.8e-95;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 EFMKKTATAIAVALAGFATVAADIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAMY 60
DB 1 EFMKKTATAIAVALAGFATVAADIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAMY 60
QY 61 OQPGQAPRLILYGASTATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYQSSSPQ 120
DB 61 OQPGQAPRLILYGASTATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYQSSSPQ 120
QY 121 TPQITFGGGTKVEIKRTVAAPSVSGSGSGSGSQVQLVPSGGSVVPQGRSLRLIS 180
DB 121 TPQITFGGGTKVEIKRTVAAPSVSGSGSGSGSQVQLVPSGGSVVPQGRSLRLIS 180
QY 181 CAASGPPRSPFAMHWVRQALGKLEWNAVISTDSTKYAASVKGRFTISRDTSKNTVYL 240
DB 181 CAASGPPRSPFAMHWVRQALGKLEWNAVISTDSTKYAASVKGRFTISRDTSKNTVYL 240
QY 241 KNSLRTEDTAVYYCARQDSLLGDYDHYGLDVGWKGITTVYSSGSEQKLISEEDLNHHH 300
DB 241 KNSLRTEDTAVYYCARQDSLLGDYDHYGLDVGWKGITTVYSSGSEQKLISEEDLNHHH 300
QY 301 HKKL 304
DB 301 HKKL 304

RESULT 3
US-09-782-397-17
; Sequence 17, Application US/09782397
; Publication No. US20030021779A1
; GENERAL INFORMATION:
; APPLICANT: Maici, Michael D.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT
; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESS: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,397
; FILING DATE: 13-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/862,124
; FILING DATE: 1997-05-22
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
```

US-09-782-397-17

Query Match 92.3%; Score 1460.5; DB 10; Length 287;  
Beet Local Similarity 93.8%; Pred. No. 1.4e-87;  
Matches 285; Conservative 0; Mismatches 2; Indels 17; Gaps 1;

Qy 1 EFMKTAIAIVAGPATVAQADIVLTQSPTLSLSPGERATLSCRASQSVSSSYLAMY 60  
Db 1 EFMKTAIAIVAGPATVAQADIVLTQSPTLSLSPGERATLSCRASQSVSSSYLAMY 60  
Qy 61 QOKPGQARLLIYGASTATGMPDRFSGSGGCTDFTLTISRLEPDPFAVYYCOQYGSBPQ 120  
Db 61 QOKPGQARLLIYGASTATGMPDRFSGSGGCTDFTLTISRLEPDPFAVYYCOQYGSBPQ 120  
Qy 121 TPQITFGGCTKVEIKRTVAAPSVSQGGSGGSGGSGGQVQVLSGGGQVQPGRSRLRS 180  
Db 121 TPQITFGGCTKVEIKRTVAAPSVSQGGSGGSGGSGGQVQVLSGGGQVQPGRSRLRS 163  
Qy 181 CAASGPPRSPAMHWNRQALGKLEWAVISYDGSSTKYAASVKRFTISRDTSKNTVYL 240  
Db 164 CAASGPPRSPAMHWNRQALGKLEWAVISYDGSSTKYAASVKRFTISRDTSKNTVYL 223  
Qy 241 KMSLRTEDTAVYYCARDQSLGDYDHYGLDWMKGKTTVYSSSQEQLISEEDLNHHH 300  
Db 224 KMSLRTEDTAVYYCARDQSLGDYDHYGLDWMKGKTTVYSSSQEQLISEEDLNHHH 283  
Qy 301 HHKL 304  
Db 284 HHKL 287

RESULT 4

US-10-651-453-17  
; Sequence 17, Application US/10651453  
; Publication No. US20040091484A1

; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; APPLICANT: Maltl, Pradip K.  
; APPLICANT: Kaplan, Howard A.  
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS,  
; TITLE OF INVENTION: NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PRO  
; FILE REFERENCE: 316082000103  
; CURRENT APPLICATION NUMBER: US/10/651,453  
; CURRENT FILING DATE: 2003-08-29  
; PRIOR APPLICATION NUMBER: US 09/782,397  
; PRIOR FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: US 08/862,124  
; PRIOR FILING DATE: 1997-05-22  
; PRIOR APPLICATION NUMBER: US 08/657,449  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 287  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-651-453-17

Query Match 92.3%; Score 1460.5; DB 15; Length 287;  
Beet Local Similarity 93.8%; Pred. No. 1.4e-87;  
Matches 285; Conservative 0; Mismatches 2; Indels 17; Gaps 1;

Qy 1 EFMKTAIAIVAGPATVAQADIVLTQSPTLSLSPGERATLSCRASQSVSSSYLAMY 60  
Db 1 EFMKTAIAIVAGPATVAQADIVLTQSPTLSLSPGERATLSCRASQSVSSSYLAMY 60  
Qy 61 QOKPGQARLLIYGASTATGMPDRFSGSGGCTDFTLTISRLEPDPFAVYYCOQYGSBPQ 120  
Db 61 QOKPGQARLLIYGASTATGMPDRFSGSGGCTDFTLTISRLEPDPFAVYYCOQYGSBPQ 120  
Qy 121 TPQITFGGCTKVEIKRTVAAPSVSQGGSGGSGGSGGQVQVLSGGGQVQPGRSRLRS 180  
Db 121 TPQITFGGCTKVEIKRTVAAPSVSQGGSGGSGGSGGQVQVLSGGGQVQPGRSRLRS 180

Db 121 TPQITFGGCTKVEIKRTVAAPSVSQGGSGGSGGSGGQVQVLSGGGQVQPGRSRLRS 163

Qy 181 CAASGPPRSPAMHWNRQALGKLEWAVISYDGSSTKYAASVKRFTISRDTSKNTVYL 240  
Db 164 CAASGPPRSPAMHWNRQALGKLEWAVISYDGSSTKYAASVKRFTISRDTSKNTVYL 223  
Qy 241 KMSLRTEDTAVYYCARDQSLGDYDHYGLDWMKGKTTVYSSSQEQLISEEDLNHHH 300  
Db 224 KMSLRTEDTAVYYCARDQSLGDYDHYGLDWMKGKTTVYSSSQEQLISEEDLNHHH 283  
Qy 301 HHKL 304  
Db 284 HHKL 287

RESULT 5

US-09-203-958A-2

; Sequence 2, Application US/09203958A  
; Publication No. US20030039641A1

; GENERAL INFORMATION:  
; APPLICANT: Keler, Tibor  
; APPLICANT: GOLDSTEIN, Joel  
; APPLICANT: GRAZIANO, Robert  
; APPLICANT: DEO, Vashant M.  
; TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR  
; TITLE OF INVENTION: BINDING COMPONENTS  
; FILE REFERENCE: MXI-099CPA  
; CURRENT APPLICATION NUMBER: US/09/203,958A  
; CURRENT FILING DATE: 1998-12-02  
; PRIOR APPLICATION NUMBER: 60/067232  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-09-203-958A-2

Query Match 58.7%; Score 928; DB 10; Length 352;  
Beet Local Similarity 66.4%; Pred. No. 8.3e-53;  
Matches 192; Conservative 26; Mismatches 45; Indels 26; Gaps 5;

Qy 18 ATVAQADIVLTQSPTLSLSPGERATLSCRASQSV-----SSSYLAMYQOKPGQARLLI 72  
Db 32 AQPASDIDLQTPSPESLSASVGDRTITCKSSQSVLVSNNQNYLAWYQOKPGKAPKLLI 91  
Qy 73 YGASTRATGMPDRFSGSGGCTDFTLTISRLEPDPFAVYYCOQYGSBPOTPOITFGGCTKV 132  
Db 92 YWASTRESGVPSRFSGSGGCTDFTLTISRLEPDPFAVYYCHQYLS-----WTFQGTGV 146  
Qy 133 EIKRTVAAPSVSQGGSGGSGGSGGQVQVLSGGGQVQPGRSRLSCASGPPRPSRA 192  
Db 147 EIKS-----SGGGSGGSGGSGGSEVOLVESGGGQVQPGRSRLSCSSSGFTPSDNY 199  
Qy 193 MHWNRQALGKLEWAVISYDGSSTKYAASVKRFTISRDTSKNTVYLKMSLRTEDPFAV 252  
Db 200 MHWNRQALGKLEWAVISYDGSSTKYAASVKRFTISRDTSKNTVYLCQMDLRREDTCV 259  
Qy 253 YTCARDQSLGDYDHYGLDWMKGKTTVYSSG-----SEQKLISEEDLN 297  
Db 260 YFCAR-----GYRREYEGAMDYWGQGTPTVSSPRLQVDEQKLISEEDLN 303

RESULT 6

US-10-634-862-11

; Sequence 11, Application US/10634862  
; Publication No. US20040048383A1  
; GENERAL INFORMATION:  
; APPLICANT: RUDERT, FRITZ  
; APPLICANT: GE, LIMING

```
APPLICANT: ILAG, VIC
TITLE OF INVENTION: NOVEL METHOD AND PHAGE FOR THE IDENTIFICATION OF
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIC
FILE REFERENCE: MORPHO/9
CURRENT APPLICATION NUMBER: US/10/634,862
CURRENT FILING DATE: 2003-08-06
PRIOR APPLICATION NUMBER: US/09/495,880A
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: PCT/EP98/04836
PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: EP 97 11 3319.4
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 456
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ompA-FLAG-scFv (anti-
US-10-634-862-11
```

```
Query Match          58.6%; Score 926.5; DB 15; Length 456;
Best Local Similarity 63.1%; Pred. No. 1.3e-52;
Matches 190; Conservative 37; Mismatches 49; Indels 25; Gaps 6;
```

```
QY 3 MKKTAIAVALAGPATAQA---DIVLTQSPGTLSPGERATLSCRAQSQSSS--- 55
DB 1 MKKTAIAIAVALAGPATAQAADYKDIQMTQSPSLVTAGEKVTMSCTSSQSLFNSGKX 60
QY 56 -FLAWYQQRGAPRLITIGASTRATGMDRPSGSSGSDFTLTISRLEPEFAVYCCQ 114
DB 61 NLTLYQQPQPPKPLIYMASTRGVDREFTSGSGSDFTLTISRVAEDLAVYYCQN 120
QY 115 YGSSPQTPTFGGKTKVEIKRTVAAP-----VSGGSGSGSGSGSGSGSOVLVS 166
DB 121 DYSNP---LTRGGGFKLELRKAGGGSGSGSGSGSGSGSGSGSGSGSEVQLVRS 176
QY 167 GGGVVOQGRSLRLSCAASGFPFRSFAMHWROALGKLEWVAIVSYDSTKTYADSVKGR 226
DB 177 GGDLYVPGGSLKSLSCAASGFSFSYGMWVRQTDPKRLIEWALTISNGGAYTYPDSVKGR 236
QY 227 FTISDTSNTYLYLKMNSLRTEDTAVYCARQSLGDVDHYGDLWVGKGTYYVSSGS 286
DB 237 FTISDNMAKNTLYLQMSLSKSDSAMYCARR-----YDE-NGPAYWGQGLTVTSASG 291
QY 287 E 287
DB 292 E 292
```

```
RESULT 7
US-09-983-580-6
Sequence 6, Application US/09983580
Patent No. US20020151061A1
GENERAL INFORMATION:
APPLICANT: Filpula, David R.
APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. US20020151061A1 Method for Targeted Delivery of Nucleic Acid
FILE REFERENCE: 0977.2300002
CURRENT APPLICATION NUMBER: US/09/983,580
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 09/420,592
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 283
```

```
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Kabat
OTHER INFORMATION: Consensus
NAME/KEY: UNSURE
LOCATION: (232)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (234)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (239)
OTHER INFORMATION: May be any amino acid.
US-09-983-580-6
```

```
Query Match          56.4%; Score 892; DB 9; Length 283;
Best Local Similarity 66.3%; Pred. No. 1.5e-50;
Matches 181; Conservative 29; Mismatches 47; Indels 16; Gaps 5;
```

```
QY 24 DIVLTQSPGTLSPGERATLSCRAQSV--SSYLAWYQQRGAPRLITIGASTRATG 81
DB 1 DIQMTQSPSLASAVGDHVTITCRASQSLVSIWLAHYQQRKAPRLIYAASLSLRS 60
QY 82 MPDRSGSGSDFTLTISRLEPEFAVYCCQYQSSPQTPTFGGKTKVEIKRTVAAP 141
DB 61 VPSRPSGSGSDFTLTISRLEPEFAVYCCQYNS--LPEWTFGQTKVEIKGS--- 113
QY 142 SVSGGSGSGSGSGSGSGSQVLVSGGQVOPGRSLRLSCAASGFPFRSFAMHWROALG 201
DB 114 --TSGSGRSGSGSGTKEVQLVSGGGLVOPGSLRLSCAASGFSYAMSWVRQAPG 171
QY 202 KGLEWVAIVS--YDSTKTYADSVKGRFTISRDTSKNTYLYLKMNSLRTEDTAVYCCAQ 259
DB 172 KGLEWVAIVSISGKTGGSYTYADSVKGRFTISRDNKNTLYLQMSLSRAEDTAVYCAAGR 231
QY 260 ---SLGPDHYGDLWVGKGTYYVSSGSRK 289
DB 232 XGSLSGKYYHYHFDYWGQGLTVTSKRRK 264
```

```
RESULT 8
US-09-985-442-6
Sequence 6, Application US/09985442
Patent No. US20020156248A1
GENERAL INFORMATION:
APPLICANT: Filpula, David R.
APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic Acid
FILE REFERENCE: 0977.2300003
CURRENT APPLICATION NUMBER: US/09/985,442
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/420,592
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 283
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Kabat
OTHER INFORMATION: Consensus
NAME/KEY: UNSURE
LOCATION: (232)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (234)
OTHER INFORMATION: May be any amino acid.
NAME/KEY: UNSURE
LOCATION: (239)
OTHER INFORMATION: May be any amino acid.
```

```

LOCATION: (229)
OTHER INFORMATION: May be any amino acid.
US-09-985-442-6

Query Match      56.4%; Score 892; DB 9; Length 283;
Best Local Similarity    66.3%; Pred. No. 1.5e-50;
Matches   181; Conservative     29; Mismatches   47; Indels   16; Gaps    5;

QY          24 DIVLTQSFGTSLSPGEFATLSCRASGV--SSSTLYNQOKPGCAPLLIYGASTRATG  81
           |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB          1 DIOMTGSPSSLASVGDRTVTTCRAAGSLVISNVLAWYOQRKPKAPKLIIYAASSLSGG  60

QY          82 MPDRPSGSCTDPTLTRISLEPEDFAYNYOOQGSSQTQGITFEGETTKIEIKRYAAP  141
           VPSRPSSSGSSTDFTPLTTISSLPDEFATYYCOQNNS--LFEMTFGGGTKEIKIGS----  113

QY          142 SVSGCGGSGGSGGSGGSOVOLVSNGGWOPGRSLRLSCAAGFPFRPFMHWRQLG  201
           :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB          114 --TSGSKRGSGEGESTKGEOVLVESGGGLVPGGSLRLSCAAGFTPFSVMWVRQA RG  171

QY          202 KGLEMWAVIS--YDGSTRKYADSVKGRETTISRDTISKNTVIKKMSLRATEDTAIVYYYCARDQ  259
           |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB          172 KGLEWMVASISKTDPGSTTYADVSYKRETIIRDNSKNTLYLQMNSSLRADTPAAVVYCCARG  231

QY          260 ---SLGDIHYHTELDVGAKGYTVTVSSGSRCK  289
           |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB          232 XGXSLGXYHHFYHDWGOGTLTVTSSKKKKK  264


RESULT 9
US-09-956-086-3
Sequence 3, Application US/09956086
Patent No. US20020155498A1
GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
            WANG, MAOLIANG
            SHORR, ROBERT
            WHITLOW, MARC
            LEE, LIHSYNG S.

TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
                  CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,086
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600

```

```

1 TELEFAX: (202)371-2540
2
3 INFORMATION FOR SEQ ID NO: 3:
4
5 SEQUENCE CHARACTERISTICS:
6
7 LENGTH: 263 amino acids
8
9 TYPE: amino acid
10
11 STRANDEDNESS: single
12
13 TOPOLOGY: No. US2002015498A1 Relevant
14
15 MOLECULE TYPE: peptide
16
17 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
18
19 US-09-956-086-3
20
21 Query Match 56.1%; Score 887; DB 9; Length 263;
22 Best Local Similarity 67.2%; Pred. No. 2,9e-50;
23 Matches 180; Conservative 27; Mismatches 45; Indels 16; Gaps 5;
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
```

1 PILING DATE: 30-APR-1997  
 2 ATTORNEY/AGENT INFORMATION:  
 3 NAME: KIM, JUDITH U.  
 4 REGISTRATION NUMBER: 40,679  
 5 REFERENCE/DOCKET NUMBER: 0977.2280003  
 6 TELECOMMUNICATION INFORMATION:  
 7 TELEPHONE: (202)371-2600  
 8 TELEFAX: (202)371-2540  
 9 INFORMATION FOR SEQ ID NO: 3:  
 10 SEQUENCE CHARACTERISTICS:  
 11 LENGTH: 263 amino acids  
 12 TYPE: amino acid  
 13 STRANDEDNESS: single  
 14 TOPOLOGY: not relevant  
 15 MOLECULE TYPE: peptide  
 16 SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 17 DS-09-956-087-3



```
RESULT 13
US-10-422-628-43
; Sequence 43, Application US/10422628
; Publication No. US20040014174A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: MAYFIELD, Stephen P.
; APPLICANT: FRANKLIN, Scott E.
; TITLE OF INVENTION: EXPRESSION OF POLYPEPTIDES IN CHLOROPLASTS, AND COMPOSITIONS AND
; TITLE OF INVENTION: FOR EXPRESSING SAME
; FILE REFERENCE: SCRIPI510-2
; CURRENT APPLICATION NUMBER: US/10/422,628
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/375,129
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/434,957
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-628-43

Query Match          54.6%; Score 863.5; DB 15; Length 277;
Best Local Similarity 67.5%; Pred. No. 1,1e-48;
Matches 179; Conservative 24; Mismatches 49; Indels 13; Gaps 4;

QY 20 VAQ-ADIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASTR 78
DB 3 VAQAASSLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASSR 62
QY 79 ATGMPDRSSGSGGDTFTLTISRLPEDEPAVYCCQYSSSPQTPTGGGKVEIKRTV 138
DB 63 ATGIPDRSSGSGGDTFTLTISRLPEDEPAVYCCQYSSP---TTGGGKVEIKRT- 116
QY 139 AAPVSGSGSGSGSGGSGQVQLVESGQVGPGRSLRLSCAASGFPFRSPAMHWYRQ 198
DB 117 ----SSGGSGSGG--GGGSSRSLSLQSGAEVKKRQSVKYSYCRASGSGSFSAINWYRQ 170
QY 199 ALGKLEWAVIISYDSTKYVADSVKGRFTISRDTSKNTVYIKMNSLTREDPAVYVCARD 258
DB 171 AQQGGLWGMGILMIFGTTNYAQKFKQDRLITADVSTSTAWMQLSGLTYPEDTAMVYCARV 230
QY 259 QSLGDDYHYGGLDVGWKGTTVTVS 283
DB 231 AYMLEPTVAGLDVWKGKTTVTVS 255

RESULT 14
US-10-409-938-21
; Sequence 21, Application US/10409938
; Publication No. US20030219733A1
; GENERAL INFORMATION:
; APPLICANT: Clark et al.
; TITLE OF INVENTION: ANTI-BODY GENE TRANSFER AND RECOMBINANT AAV THEREFOR
; FILE REFERENCE: 2835/53282
; CURRENT APPLICATION NUMBER: US/10/409,938
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/371,501
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-409-938-21

Query Match          54.2%; Score 857.5; DB 15; Length 279;
```

```
Best Local Similarity 65.3%; Pred. No. 2.6e-48;
Matches 179; Conservative 22; Mismatches 46; Indels 27; Gaps 6;

QY 23 ADIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASTRATGM 82
DB 21 ADIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASTRANGI 80
QY 83 PDRFSGSGSGTDFTLTISRLEPEDPAVYCCQYSSSPQTPTGGGKVEIKRTVAAPS 142
DB 81 PDRFSGSGSGTDFTLTISRLEPEDPAVYCCQYSSP-----YTFQGTTRKVIKR----- 130
QY 143 VSGGSGSGSGSGGGG---SQVQLVESGGGVQVQPSRLRLSCAASGFPFRSPAMHWYQA 199
DB 131 --GGGSGSGSGSGSGGSSQVQLVQSGAEVKKRQSVVQVCKASGKGTFSMIGFWYRQA 188
QY 200 LGKLEWAVIISYDSTKYVADSVKGRFTISRDTSKNTVYIKMNSLTREDPAVYVCARDQ 259
DB 189 PCKGLEWVGIIIPFGISNYAQKGRGRTFTADQATSTAWMLTNLRDQDTAVYVCARD- 247
QY 260 SLG---DYDHYG---LDVWKGTTVTVS 284
DB 248 --FGPDWEDGSDYDGGSGRFGDFWGGGTLVTVS 279

RESULT 15
US-10-423-847-10
; Sequence 10, Application US/10423847
; Publication No. US20040009166A1
; GENERAL INFORMATION:
; APPLICANT: FILIPULA, DAVID RAY
; APPLICANT: YANG, KAREN
; APPLICANT: BASU, AMARTYA
; APPLICANT: WANG, MAOLIANG
; TITLE OF INVENTION: SINGLE CHAIN ANTIGEN-BINDING POLYPEPTIDES FOR POLYMER
; TITLE OF INVENTION: CONJUGATION
; FILE REFERENCE: 213.1180
; CURRENT APPLICATION NUMBER: US/10/423,847
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 09/791,578
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/791,540
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/069,842
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/044,449
; PRIOR FILING DATE: 1997-04-30
; PRIOR APPLICATION NUMBER: 60/050,472
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 60/063,074
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/067,341
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic 2-7-SC-1
; OTHER INFORMATION: Protein sequence
US-10-423-847-10

Query Match          53.7%; Score 849.5; DB 15; Length 252;
Best Local Similarity 60.9%; Pred. No. 7.8e-48;
Matches 170; Conservative 31; Mismatches 51; Indels 27; Gaps 5;

QY 24 DIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYGASTRATGM 83
DB 1 DIQWTQSPSSLSASVGRVITTCRASQGI-RNYLAWYQKPGKAPKLIYAASLTQSGVP 59
QY 84 DRFGSGSGGTDFTLTISRLEPEDPAVYCCQYSSSPQTPTGGGKVEIKRTVAAPS 143
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2005, 08:46:53, Search time 24 Seconds  
(without alignments)  
1218.746 Million cell updates/sec

Title: US-09-194-164-14  
Perfect score: 1582  
Sequence: 1 EFMKKTALIAVALAGPATV.....GSEQKLSIEDLNHHHKKL 304

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR 79: \*  
1: P1r1.\*  
2: P1r2.\*  
3: P1r3.\*  
4: P1r4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541.5	34.2	122	2 E36005	Ig heavy chain V r
2	539.5	34.1	128	2 S48797	Ig heavy chain V r
3	537.5	34.0	215	2 A23746	Ig kappa chain V-I
4	534	33.8	109	2 G30607	Ig kappa chain V-I
5	530	33.5	109	2 A30608	Ig kappa chain V-I
6	530	33.5	109	2 B30601	Ig kappa chain V-I
7	529	33.4	109	2 D30601	Ig kappa chain V-I
8	528.5	33.4	108	2 H44151	Ig kappa chain V r
9	527.5	33.3	215	2 JE0242	Ig kappa chain V r
10	527	33.3	109	2 C30601	Ig kappa chain V-I
11	526	33.2	109	2 F30607	Ig kappa chain V-I
12	526	33.2	129	1 K3H08A	Ig kappa chain pre
13	525	33.2	123	2 S38493	Ig heavy chain - h
14	525	33.2	129	2 S49532	anti-Sm antibody V
15	524	33.1	109	2 H30601	Ig kappa chain V-I
16	523	33.1	109	1 K3H08T	Ig kappa chain V-I
17	522.5	33.0	114	2 S46375	Ig kappa chain V-I
18	522	33.0	109	2 PH0963	Ig kappa chain V r
19	521	32.9	109	2 G30601	Ig kappa chain V r
20	520	32.9	129	1 K3H08T	Ig kappa chain pre
21	518	32.7	108	2 C30608	Ig kappa chain V-I
22	516	32.6	129	2 S46369	Ig light chain var
23	516	32.6	134	2 S38643	Ig kappa chain V r
24	515	32.6	107	2 PH0965	Ig kappa chain V r
25	514	32.5	108	2 B30608	Ig kappa chain V-I
26	514	32.5	145	2 S20631	Ig kappa chain - h
27	513	32.4	119	2 F30605	Ig heavy chain V r
28	512	32.4	109	2 F30601	Ig kappa chain V-I
29	510.5	32.3	104	2 PH0964	Ig kappa chain V r

30	510	32.2	109	1 K3H08T	Ig kappa chain V-I
31	510	32.2	128	2 S20636	Ig kappa chain V r
32	509	32.1	121	2 G36005	Ig heavy chain V r
33	508	32.1	134	2 S31679	Ig heavy chain V r
34	507.5	32.1	110	2 E30607	Ig kappa chain V-I
35	507.5	32.1	114	2 S46390	Ig heavy chain V r
36	507.5	32.1	147	2 I37780	Ig variable region
37	506	32.0	109	1 K3H08T	Ig kappa chain V-I
38	505	31.9	109	2 F44151	Ig kappa chain V r
39	504.5	31.9	122	2 S31117	Ig heavy chain - h
40	504	31.9	132	2 S31603	Ig heavy chain V r
41	503.5	31.8	108	2 E30609	Ig kappa chain V-I
42	503	31.8	130	2 PH0968	Ig heavy chain pre
43	503	31.8	133	2 A49028	Ig heavy chain V-I
44	502.5	31.8	110	2 S44120	Ig kappa chain V-I
45	502	31.7	121	2 S40327	Ig kappa chain - h

ALIGNMENTS

```
RESULT 1
E36005
Ig heavy chain V region (M72) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: E36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90345571; PMID:2117273
A:Accession: E36005
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <SCH>
A:Cross-references: GB:M34030
C:Genetics:
A:Gene: GDB:IGH@; IGHDI1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      34.2%; Score 541.5; DB 2; Length 122;
Best Local Similarity 84.0%; Pred. No. 4.4e-30;
Matches 105; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

QY 160 QVQLVESGGGVVQPGSRSLRSCAASGFPFRSPAMHWVRQALGKLEWVAIVSYDSTKY 219
    |||||
DB 1 QVQLVESGGGVVQPGSRSLRSCAASGFTFSYAMHWVRQAPKGLWVAIVSYDGSNKY 60
    |||||

QY 220 ADSVYKGRFTISRDTSKNTVYLKMSISLTEDTAIVVYCARDOSLGSDYHYGGLDVGKGT 279
    |||||
DB 61 ADSVYKGRFTISRDTSKNTVYLQMSISLTEDTAIVVYCAADRH---SSSWYIGMDVWGCGTT 117
    |||||

QY 280 VTVSS 284
    |||||
DB 118 VTVSS 122
    |||||

RESULT 2
S48797
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
R:Mamoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S48797
A:Molecule type: mRNA
```

A:Residues: 1-128 <MAH>  
A:Cross-references: EMBL:246379; NID:g587147; PIDN:CAA86512.1; PID:g1340168  
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A:Title: The repertoire of human germ-line V(H) sequences reveals about fifty groups of V  
A:Reference number: S26885; MUID:93021117; PMID:1404388  
A:Accession: S26893  
A:Molecule type: DNA  
A:Residues: 1-98 <TOM>  
A:Cross-references: EMBL:212350; NID:g32922; PIDN:CAA78220.1; PID:g32923  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 34.1%; Score 539.5; DB 2; Length 128;  
Best Local Similarity 82.0%; Pred. No. 6.3e-30;  
Matches 105; Conservative 6; Mismatches 14; Indels 3; Gaps 1;

QY 160 QVQLVESGSGGVQPGPSRLSCAASGFPFRSPAMHWRAALGKLEWAVISYDSTKYY 219  
DB 1 QVQLVESGSGGVQPGPSRLSCAASGFTSYGMHWRAQPKGLEWAVIYDGSNKYY 60  
QY 220 ADSVAGRFITSDTSKNLYLKNNSLRTEDTAVYYCARDQ---SLTGDYHYGLDVMGK 276  
DB 61 ADSVAGRFITSDTSKNLYLQMSLRADTAIVYCARNNYYDSSGYIYYGMDVMGQ 120  
QY 277 GTTVTVSS 284  
DB 121 GTTVTVSS 128

RESULT 3  
A23746  
Ig kappa chain V-III (Kau cold agglutinin) - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
A:Accession: A23746  
J:Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991  
A:Title: The primary structure of the Fab fragment of protein Kau, a monoclonal immunogl  
A:Reference number: A23746; MUID:91131575; PMID:1993660  
A:Accession: A23746  
A:Molecule type: protein  
A:Status: preliminary  
A:Residues: 1-215 <LBO>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 34.0%; Score 537.5; DB 2; Length 215;  
Best Local Similarity 58.7%; Pred. No. 1.5e-29;  
Matches 128; Conservative 13; Mismatches 50; Indels 27; Gaps 5;

QY 24 DIVLTQSPGTLSLSPGERATLSCASQSVSSSYLAWYQKPGQAPRLIYGASTRATGMP 83  
DB 1 EIVLTQSPATLSLSPGERATLSCASQSVSSSYLAWYQKPGQAPRLIYGASTRATGIP 60  
QY 84 DRFGSGSGTDFTLTISRLEPEDFAVYYCQOYGSSPQRTPTFGSGTKVEIKR 143  
DB 61 DRFGSGSGTDFTLTISRLEPEDFAVYYCQOYGSSP---LTFGSGTKVEIKR 116  
QY 144 SGGGSGGGSGGGSGGVQVQPGPSRLSCAASGFPFRSPAMHW-VAQALGK 202  
DB 117 FIFPSPDQKSGTASVGL-----NNFYREAKVQMKDNLQS 157  
QY 203 GLEWVAVISYDSTKYYAVSVKGRFTISR-DTSKNTVY 239  
DB 158 GNSGSEVTEQDSKDSY--SLSTLTLSKADYEKKHY 193

RESULT 4  
G30607  
Ig kappa chain V-III region (Kas) - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 21-Jan-2000  
A:Accession: G30607  
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon  
J. Immunol. 142, 3158-3163, 1989  
A:Title: Structural and idiotypic characterization of the L chains of human Igm autoantib  
A:Reference number: A30601; MUID:89215279; PMID:2496160  
A:Accession: G30607  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-109 <GON>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 33.8%; Score 534; DB 2; Length 109;  
Best Local Similarity 92.0%; Pred. No. 1.3e-29;  
Matches 104; Conservative 4; Mismatches 1; Indels 4; Gaps 1;

QY 24 DIVLTQSPGTLSLSPGERATLSCASQSVSSSYLAWYQKPGQAPRLIYGASTRATGMP 83  
DB 1 DIVLTQSPGTLSLSPGERATLSCASQSVSSSYLAWYQKPGQAPRLIYGASTRATGIP 60  
QY 84 DRFGSGSGTDFTLTISRLEPEDFAVYYCQOYGSSPQRTPTFGSGTKVEIKR 136  
DB 61 DRFGSGSGTDFTLTISRLEPEDFAVYYCQOYGSSP---FTFGSGTKVEIKR 109

RESULT 5  
A30608  
Ig kappa chain V-III region (Son) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
A:Accession: A30608  
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon  
J. Immunol. 142, 3158-3163, 1989  
A:Title: Structural and idiotypic characterization of the L chains of human Igm autoantib  
A:Reference number: A30601; MUID:89215279; PMID:2496160  
A:Accession: A30608  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-109 <GON>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 33.5%; Score 530; DB 2; Length 109;  
Best Local Similarity 92.0%; Pred. No. 2.3e-29;  
Matches 104; Conservative 4; Mismatches 1; Indels 4; Gaps 1;

QY 24 DIVLTQSPGTLSLSPGERATLSCASQSVSSSYLAWYQKPGQAPRLIYGASTRATGMP 83  
DB 1 EIVLTQSPGTLSLSPGERATLSCASQSVSSSYLAWYQKPGQAPRLIYGASTRATGIP 60  
QY 84 DRFGSGSGTDFTLTISRLEPEDFAVYYCQOYGSSPQRTPTFGSGTKVEIKR 136  
DB 61 DRFGSGSGTDFTLTISRLEPEDFAVYYCQOYGSSP---YTFGSGTKVEIKR 109

RESULT 6  
B30601  
Ig kappa chain V-III region (Gio) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004  
A:Accession: B30601  
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon  
J. Immunol. 142, 3158-3163, 1989  
A:Title: Structural and idiotypic characterization of the L chains of human Igm autoantib  
A:Reference number: A30601; MUID:89215279; PMID:2496160  
A:Accession: B30601  
A:Status: preliminary  
A:Molecule type: protein



```

Db      1 EIVLTQSPGTLISLSPGERATLSCRAQSQSVSSYLAWYQQRPGQAPRLLIYGASSTRATGIP 60
Qy      84 DRFGSGSGTDFTLTIISRLPEDPFAVYYCCQYGSSPQTPQTTFGGGTVEIKR 136
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 DRFGSGSGTDFTLTIISRLPEDPFAVYYCCQYGSSP-----LTFGGGTVEIKR 109

RESULT 11
F30607
Ig kappa chain V-III region (Box) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C/Accession: F30607
R/Cont.: P.R.; Chen, P.P.; McGinnis, D.; Arionilla, M.L.; Fernandez, J.; Carson, D.; Solo
U.: Immunol. 142, 3158-3163, 1989
A/Title: Structural and idotypic characterization of the L chains of human IGM autoanti
A/Reference number: A30601; MWID:89215279; PMID:2496160
A/Accession: F30607
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-109 <CON>
A/Cross-references: UNIPROT:Q9UL78
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match      33.2%; Score 526; DB 2; Length 109;
Best Local Similarity 91.2%; Pred. No. 4,3e-29;
Matches 103; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

Qy      24 DIVLTQSPGTLISLSPGERATLSCRAQSQSVSSYLAWYQQRPGQAPRLLIYGASTRATGMP 83
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EIVLTQSPGTLISLSPGERATLSCRAQSQSVSSYLAWYQQRPGQAPRLLIYGASSTRATGIP 60

Qy      84 DRFGSGSGTDFTLTIISRLPEDPFAVYYCCQYGSSPQTPQTTFGGGTVEIKR 136
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 DRFGSGSGTDFTLTIISRLPEDPFAVYYCCQYGSSPQTPQTTFGGGTVEIKR 109

RESULT 12
K3H0HA
Ig kappa chain precursor V-III region (Hah) - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 03-Jul-2004
C/Accession: P10022
R/Klpps, T.O.; Tomhave, E.; Chen, P.P.; Carson, D.A.
U.: Exp. Med. 167, 840-852, 1988
A/Title: Autoantibody-associated kappa light chain variable region gene expressed in chr
A/Reference number: P10021; MWID:88171307; PMID:3127527
A/Accession: P10022
A/Molecule type: mRNA
A/Residues: 1-129 <KIP>
A/Cross-references: UNIPROT:P18135
C/Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed i
C/Genetics:
A/Gene: GDB:IGKV3
A/Cross-references: GDB:136266
A/Map position: 2p12-2p11
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-129/Product: Ig kappa chain V-III region (Hah) #status predicted <MAT>
F:21-117/Region: V segment
F:36-111/Domain: immunoglobulin homology <IMM>
F:44-55/Region: complementarity-determining 1
F:71-77/Region: complementarity-determining 2
F:110-117/Region: complementarity-determining 3
F:118-129/Region: J segment (UK1)
F:43-109/Disulfide bonds: #status predicted

Query Match      33.2%; Score 526; DB 1; Length 129;

```

```

Best Local Similarity 91.2%; Pred. No. 5.2e-29;
Matches 103; Conservative 5; Mismatches 1; Indels 4; Gaps 1;

Qy      24 DIVLTQSPGTLISLSPGERATLSCRAQSQSVSSYLAWYQQRPGQAPRLLIYGASTRATGMP 83
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      21 EIVLTQSPGTLISLSPGERATLSCRAQSQSVSSYLAWYQQRPGQAPRLLIYGASSTRATGIP 80

Qy      84 DRFGSGSGTDFTLTIISRLPEDPFAVYYCCQYGSSPQTPQTTFGGGTVEIKR 136
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      81 DRFGSGSGTDFTLTIISRLPEDPFAVYYCCQYGSSTR-----LTFGGGTVEIKR 129

RESULT 13
S38493
Ig heavy chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S38493
R/Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Fimern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
Submitted to the EMBL Data Library, June 1993
A/Description: Human antibody fragments specific for human blood group antigens from a pi
A/Reference number: S38488
A/Accession: S38493
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-123 <MAP>
A/Cross-references: EMBL:Z23036; NID:G414033; PIDN:CAA80571.1; PID:G414034
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      33.2%; Score 525; DB 2; Length 123;
Best Local Similarity 83.2%; Pred. No. 5.8e-29;
Matches 104; Conservative 5; Mismatches 14; Indels 2; Gaps 1;

Qy      160 QVQLVESGGGVQVQGRSLRLSCAASGFPFRFAHWRAQALGKLEWAVTSYGSTCY 219
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 QVQLQESGGGVQVQGRSLRLSCAASGFTFSYAHMWRAQAKGLEWAVLSTGSKNKY 60

Qy      220 ADYVKGRTISRDTSKNTVYLKMSLRTEDTAVYYCARDQSLGDYHYGLDVWKGKTT 279
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 ADYVKGRTISRDNKNTLYQNMSLRAEDTAVYYCARARSNMYY--YYMDVWKGKTT 118

Qy      280 VTSS 284
        :|||||
Db      119 VTSS 123

RESULT 14
S49532
anti-Sm antibody VL chain (V kappa 3/J kappa 2) - human
C/Species: Homo sapiens (man)
C/Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C/Accession: S49532
R/Mahmoudi, M.; Edgars, J.; Cairns, E.; Bell, D.
Submitted to the EMBL Data Library, October 1994
A/Description: Molecular characterization of natural human anti-Sm autoantibodies.
A/Reference number: S48797
A/Accession: S49532
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-129 <MAH>
A/Cross-references: EMBL:Z46345; NID:9560843; PIDN:CAA86464.1; PID:9560844
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-111/Domain: immunoglobulin homology <IMM>

Query Match      33.2%; Score 525; DB 2; Length 129;
Best Local Similarity 91.2%; Pred. No. 6.1e-29;
Matches 103; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

Qy      24 DIVLTQSPGTLISLSPGERATLSCRAQSQSVSSYLAWYQQRPGQAPRLLIYGASTRATGMP 83
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      21 EIVLTQSPGTLISLSPGERATLSCRAQSQSVSSYLAWYQQRPGQAPRLLIYGASSTRATGIP 80

```

QY 84 DRFGSGSGTDTFTLTISRLEPEDPAVYCCQYGSSTPQTITFGGKVEIKR 136  
 |||||||  
 DB 81 DRFGSGSGTDTFTLTISRLEPEDPAVYCCQYGSSTPQ---TFGGKTLKIKR 129  
 |||||||

## RESULT 15

H30601  
 Ig kappa chain V-II region (Gar and Flo) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 29-Jun-1989 #sequence \_revision 29-Jun-1989 #text\_change 21-Jan-2000  
 C/Accession: H30601; E30601  
 R/Goni, P.R.; Chen, P.P.; McGinlis, D.; Arjonnilla, M.L.; Fernandez, J.; Carson, D.; Sold  
 J. Immunol. 142, 3158-3163, 1989  
 A/Title: Structural and idiotypic characterization of the L chains of human IgM autoantib  
 A/Reference number: A30601; MUID:89215279; PMID:2496160  
 A/Accession: H30601  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-109 <GONI>  
 A/Accession: E30601  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-109 <GONI>  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/16-91/Domain: immunoglobulin homology <IM>

Query Match 33.1%; Score 524; DB 2; Length 109;  
 Best Local Similarity 91.2%; Pred. No. 5, 9e-29;

Matches 103; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 24 DIVLTQSPGTLISPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLIYGASTRATQMP 83  
 :|||||  
 DB 1 EIVLTQSPGTLISPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLIYGASSRATGIP 60  
 :|||||

QY 84 DRFGSGSGTDTFTLTISRLEPEDPAVYCCQYGSSTPQTITFGGKVEIKR 136  
 |||||||  
 DB 61 DRFGSGSGTDTFTLTISRLEPEDPAVYCCQYGSSTP---YTFGGKTLKIKR 109  
 |||||||

Search completed: February 18, 2005, 08:57:57  
 Job time : 25 secs

**THIS PAGE BLANK (USPTO)**